

GenCore version 5.1.8
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OM protein - protein search, using SW model

Run on: May 20, 2006, 20:15:01 ; Search time 84 seconds
(without alignments)
789.243 Million cell updates/sec

Title: US-10-705-716A-2

Perfect score: 767

Sequence: MGCGGSRADAEPRYTESNT.....VTEENIQRQMDRSKRVTKNCIN 145

Scoring table: BLASTM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq8;*

1: geneseq1980s;*

2: geneseq1990s;*

3: geneseq2000s;*

4: geneseq2001s;*

5: geneseq2002s;*

6: geneseq2003as;*

7: geneseq2003bs;*

8: geneseq2004as;*

9: geneseq2005s;*

10: geneseq2006s;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	767	100.0	145	ADO48473
2	746	97.3	145	ADO48479
3	645	84.1	145	AAB95018
4	645	84.1	145	AHQ19498
5	645	84.1	145	ABP18646
6	645	84.1	145	ADC31800
7	645	84.1	145	ADM46959
8	645	84.1	145	ADP48475
9	617.5	80.5	180	ADM46961
10	473.5	61.7	149	ADM46963
11	335.5	43.7	92	ADQ81902
12	294	38.3	54	ADQ48481
13	288	37.5	73	ADM46962
14	278	36.2	54	ADM46960
15	278	36.2	54	ADQ48477
16	272	35.5	80	ADM46964
17	140	18.3	25	ADM46979
18	99	12.9	18	ADM46977
19	92.5	12.1	78	ADM13456
20	89	11.6	16	ADQ48482
21	87.5	11.4	260	ABG09899
22	87.5	11.4	592	ABG15607
23	85.5	11.1	4	ADQ15607
24	85.5	11.1	274	ADY09773

ALIGNMENTS

RESULT 1	ADO48473	ADO48473 standard; protein, 145 AA.
XX	ADO48473;	
XX	12-AUG-2004	(first entry)
XX	DB	Rat PTH responsive gene protein.
XX	XX	PTH responsive gene; PAIGB; bone-forming; bone; bone density modulation; transgenic animal; osteopathic; gene therapy; osteoporosis; rat.
OS	Rattus sp.	
XX	PN	WO2004044152-A2.
XX	PD	27-MAY-2004.
XX	PR	10-NOV-2003; 2003WO-US035655.
PR	12-NOV-2002; 2002US-0425532P.	
XX	PA	(AMHP) WYETH.
PI	Robinson JA, Stojanovic-Susulic V, Babij P, Murrills RJ,	
XX	DR	WPI: 2004-420299/39.
XX	N-PSDB; ADQ48472.	
PT	New nucleic acid fragment encoding a PAIGB polypeptide, useful in preparing a composition for diagnosing, treating or preventing bone related disorders, e.g., osteoporosis.	
PT	The invention relates to a novel PTH responsive gene (PAIGB) fragment encoding a polypeptide. The invention further comprises: a chimeric construct comprising the isolated nucleic acid fragment operatively linked to suitable regulatory sequences; a host cell transformed with the chimeric construct; a vector comprising the nucleic acid fragment; obtaining a nucleic acid fragment encoding the polypeptide; a method for obtaining a polypeptide; detecting the presence of the nucleic acid fragment; an antibody that specifically binds to one or more epitopes of a PAIGB polypeptide; a composition for regulating bone-forming activity in a mammal comprising the nucleic acid fragment, polypeptide or antibody.	

CC ; an agent that alters the expression of PAIGB gene or polypeptide;
 CC determining whether an agent alters the expression of PAIGB mRNA;
 CC screening agents for effectiveness in altering expression of the nucleic
 CC acid fragment; screening for agents useful for treating bone related
 CC disorders; evaluating the efficacy of a treatment of a bone related
 CC disorder in a subject; identifying polypeptides capable of binding to
 CC PAIGB; monitoring the effectiveness of treatment of a subject with a bone
 CC related agent; a transgenic animal comprising the DNA; an animal model
 CC for the study of bone density modulation comprising a first group of control
 CC animals; studying bone mass determinants; studying the modulation of bone
 CC mass; studying an effect of PAIGB on bone disorders; identifying an agent which
 CC has bone forming activity; and a stably transfected cell line comprising
 CC two constructs, the first construct comprising a ligand binding domain
 CC linked to a DNA binding domain which is linked to an activation domain
 CC all of which expression is driven by a constitutive promoter, the second
 CC construct comprising multiple copies of DNA binding elements linked to a
 CC minimal promoter which is linked to PAIGB cDNA, where upon the addition
 CC of chemical inducer, transcription of PAIGB gene is induced. The PAIGB
 CC polynucleotide has osteopathic activity. The PTH responsive gene may be
 CC used to treat disorders by gene therapy. The nucleic acid is useful in
 CC preparing a composition for diagnosing, treating or preventing bone
 CC related disorders, e.g., osteoporosis. This sequence represents a PTH
 CC responsive gene protein of the invention.

SQ Sequence 145 AA:

Query Match 100.0%; Score 767; DB 8; Length 145;

Best Local Similarity 100.0%; Pred. No. 4.9e-76; Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCGGGSRADAIPTPRYYESTWETESTWLTYTDSALPSAAATDSGPAGGLHAGVLEDP 60
 Db 1 MCGGGSRADAIPTPRYYESTWETESTWLTYTDSALPSAAATDSGPAGGLHAGVLEDP 60
 QY 61 SSNGVLRPAPPGIANPEKKKGTCOPNSOSLSSGRLTOKONGLWTEAKRDAKMSAR 120
 Db 61 SSNGVLRPAPPGIANPEKKKGTCOPNSOSLSSGRLTOKONGLWTEAKRDAKMSAR 120
 QY 121 EVAISVTEVNIRQMDSKRVTNCIN 145
 Db 121 EVAISVTEVNIRQMDSKRVTNCIN 145

SQ Sequence 145 AA:

RESULT 2 ADO48479

ID ADO48479 Standard; protein: 145 AA.

AC ADO48479;

CC DT 12-AUG-2004 (first entry)

XX DB Mouse PTH responsive gene protein.

XX KW PTH responsive gene; PAIGB; bone-forming; bone; bone density modulation;

KW transgenic animal; osteopathic; gene therapy; osteoporosis; mouse;

KW murine.

OS Mus sp.

XX PN WO2004044152-A2.

PD 27-MAY-2004.

XX PP 10-NOV-2003; 2003WO-US035655.

XX PR 12-NOV-2002; 2002US-0425532P.

PA (AMHR) WYETH.

XX PI Robinson JA, Stojanovic-Sabulic V, Babij P, Murrills RJ;

XX XX

DR WPI; 2004-420239/39.

DR N-PSDB; ADO48478.

XX PT New nucleic acid fragment encoding a PAIGB polypeptide, useful in
 PT preparing a composition for diagnosing, treating or preventing bone
 PT related disorders, e.g., osteoporosis.

PT Claim 9; SEQ ID NO 8; 169pp; English.

XX The invention relates to a novel PTH responsive gene (PAIGB) fragment
 CC encoding a polypeptide. The invention further comprises: a chimeric
 CC construct comprising the isolated nucleic acid fragment operatively
 CC linked to suitable regulatory sequences; a host cell transformed with the
 CC chimeric construct; a vector comprising the nucleic acid fragment;
 CC obtaining a nucleic acid fragment encoding the polypeptide; a method for
 CC determining whether an agent alters the expression of the nucleic acid
 CC fragment; an antibody that specifically binds to one or more epitopes of
 CC a PAIGB polypeptide; a composition for regulating bone-forming activity
 CC in a mammal comprising the nucleic acid fragment, polypeptide or antibody;
 CC ; an agent that alters the expression of PAIGB gene or polypeptide;
 CC determining whether an agent alters the expression of PAIGB mRNA;
 CC screening agents for effectiveness in altering expression of the nucleic
 CC acid fragment; screening for agents useful for treating bone related
 CC disorders; evaluating the efficacy of a treatment of a bone related
 CC disorder in a subject; identifying polypeptides capable of binding to
 CC PAIGB; monitoring the effectiveness of treatment of a subject with a bone
 CC related agent; a transgenic animal comprising the DNA; an animal model
 CC for the study of bone density modulation comprising a first group of control
 CC animals; studying bone mass determinants; studying the modulation of bone
 CC mass; studying an effect of PAIGB on bone disorders; identifying an agent which
 CC has bone forming activity; and a stably transfected cell line comprising
 CC two constructs, the first construct comprising a ligand binding domain
 CC linked to a DNA binding domain which is linked to an activation domain
 CC all of which expression is driven by a constitutive promoter, the second
 CC construct comprising multiple copies of DNA binding elements linked to a
 CC minimal promoter which is linked to PAIGB cDNA, where upon the addition
 CC of chemical inducer, transcription of PAIGB gene is induced. The PAIGB
 CC polynucleotide has osteopathic activity. The PTH responsive gene may be
 CC used to treat disorders by gene therapy. The nucleic acid is useful in
 CC preparing a composition for diagnosing, treating or preventing bone
 CC related disorders, e.g., osteoporosis. This sequence represents a PTH
 CC responsive gene protein of the invention.

SQ Sequence 145 AA:

Query Match 97.3%; Score 746; DB 8; Length 145;

Best Local Similarity 97.2%; Pred. No. 1e-73; Matches 141; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MCGGGSRADAIPTPRYYESTWETESTWLTYTDSALPSAAATDSGPAGGLHAGVLEDP 60
 Db 1 MCGGGSRADAIPTPRYYESTWETESTWLTYTDSALPSAAATDSGPAGGLHAGVLEDP 60
 QY 61 SSNGVLRPAPPGIANPEKKKGTCOPNSOSLSSGRLTOKONGLWTEAKRDAKMSAR 120
 Db 61 SSNGVLRPAPPGIANPEKKKGTCOPNSOSLSSGRLTOKONGLWTEAKRDAKMSAR 120
 QY 121 EVAISVTEVNIRQMDSKRVTNCIN 145
 Db 121 EVAISVTEVNIRQMDSKRVTNCIN 145

SQ Sequence 145 AA:

RESULT 3 AAB95018

ID AAB95018 Standard; protein: 145 AA.

AC AAB95018;

XX DT 26-JUN-2001 (first entry)

DB Human protein sequence SEQ ID NO:16726.

XX Human; primer; detection; diagnosis; antisense therapy; gene therapy.
 XX
 KW Homo sapiens.
 XX
 PN EP1074617-A2.
 XX PD 07-FEB-2001.
 XX PP 28-JUL-2000; 2000EP-00116126.
 XX PR 29-JUL-1999; 99EP-00248036.
 PR 27-AUG-1999; 99EP-00300253.
 PR 11-JAN-2000; 2000EP-0018776.
 PR 02-MAY-2000; 2000EP-00183767.
 PR 09-JUN-2000; 2000EP-00241899.
 XX PA (HELI-) HELIX RES INST.
 XX PI Oba T, Isomai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PT Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX DR WPI; 2001-318749/34.
 XX PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length PT cDNAs.
 XX PA Claim 8; SEQ ID NO 16726; 2537PP + Sequence Listing; English.
 CC The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises:
 CC (a) an oligo-dT primer and an oligonucleotide complementary to the
 CC complementary strand of a polynucleotide which comprises one of the 5602
 CC nucleotide sequences defined in the specification, where the full-length
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence is selected from those defined in the
 CC specification. The primer sets can be used in antisense therapy and in
 CC gene therapy. The primers are useful for synthesising polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH0166 to AAH3628 and
 CC AAH1363 to AAH1742 represent human cDNA sequences; AB92445 to AB9593
 CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
 CC oligonucleotides, all of which are used in the exemplification of the
 XX present invention.
 SQ Sequence 145 AA;

Query Match 84.1%; Score 645; DB 4; Length 145;
 Best Local Similarity 83.4%; Pred. No. 1.4e-62;
 Matches 121; Conservative 10; Mismatches 14; Indels 0; Gaps 0;
 QY 1 MGGGSRADATEPRYYESTWTTESWTWTTDSALPSAATDSGPEAGGLIAGVLEDGP 60
 1 MGGGSRADATEPRYYESTWTTESWTWTTDSALPSAATDSGPEAGGLIAGVLEDGP 60
 Db 1 MGGGSRADATEPRYYESTWTTESWTWTTDSALPSAATDSGPEAGGLIAGVLEDGP 60
 QY 61 SNGVLRPAPGQIANPKKMGTCGNSLSSGPIKTOKNLWTEAKDAKMSAR 120
 61 PNSGVPRSTAPGQIPKPKRVTNCIN 145
 61 PNSGVPRSTAPGQIPKPKRVTNCIN 145
 121 EVAISVTENIQDRSKRVTNCIN 145
 121 EVAISVTENIQDRSKRVTNCIN 145
 QY 121 EVAISVTENIQDRSKRVTNCIN 145
 121 EVAISVTENIQDRSKRVTNCIN 145

RESULT 4
 AAO19498
 ID AAO19498 standard; protein; 145 AA.
 XX AC AAO19498;
 XX DT 20-DEC-2002 (first entry)
 XX DE HS1 protein variant.
 XX HS1; variant; cancer; tumour; unigene cluster; cytostatic; metastasis;
 KW EST; expressed Sequence tag; colon cancer; stomach cancer; breast cancer;
 KW HS169395; HS127144; HS2; HS132793; HS3.
 XX OS Unidentified.
 XX PN Unidentified.
 PN DB1010694.A1.
 XX PD 01-AUG-2002.
 XX PR 26-JAN-2001; 2001DE-01003694.
 XX PR 26-JAN-2001; 2001DE-01003694.
 XX PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
 PT Brett D, Kemmer W;
 XX DR WPI; 2002-644835/70.
 DR N-PSDB; AAL50100.
 XX PT Diagnosis and therapy of tumors, by determining expression rates of
 CC specific expressed sequence tags of the unigene cluster, and subsequently
 CC blocking their expression.
 XX PS Claim 10; Page 5; 10PP; German.
 CC The present invention relates to the use of expressed sequence tags
 CC (ESTs), or variants, of the unique cluster HS169395 (HS1), HS127144
 CC (HS2), and/or HS132793 (HS3) for diagnosis and therapy of tumours, in
 CC which their expression rates in tumor cells and/or lymph nodes are
 CC determined. The EST Sequences are useful as prognostic markers of
 CC survival of cancer patients (high levels of EST-related mRNA are
 CC associated with a poor prognosis, specifically correlated with
 CC development of metastases); and for diagnosis and/or therapy of solid
 CC tumours, particularly of colon, stomach and breast. The present sequence
 CC is a variant of the HS1 protein shown in the exemplification of the
 CC invention.
 XX SQ Sequence 145 AA;
 Query Match 84.1%; Score 645; DB 5;
 Best Local Similarity 83.4%; Pred. No. 1.4e-62;
 Matches 121; Conservative 10; Mismatches 14; Indels 0; Gaps 0;
 QY 1 MGGGSRADATEPRYYESTWTTESWTWTTDSALPSAATDSGPEAGGLIAGVLEDGP 60
 1 MGGGSRADATEPRYYESTWTTESWTWTTDSALPSAATDSGPEAGGLIAGVLEDGP 60
 Db 1 MGGGSRADATEPRYYESTWTTESWTWTTDSALPSAATDSGPEAGGLIAGVLEDGP 60
 QY 61 SNGVLRPAPGQIANPKKMGTCGNSLSSGPIKTOKNLWTEAKDAKMSAR 120
 61 PNSGVPRSTAPGQIPKPKRVTNCIN 145
 61 PNSGVPRSTAPGQIPKPKRVTNCIN 145
 121 EVAISVTENIQDRSKRVTNCIN 145
 121 EVAISVTENIQDRSKRVTNCIN 145
 QY 121 EVAISVTENIQDRSKRVTNCIN 145
 121 EVAISVTENIQDRSKRVTNCIN 145
 RESULT 5
 ABR5846
 ID ABR58646 standard; protein; 145 AA.
 XX AC ABR58646;

CC cancer. The nucleic acids may also be used as hybridisation probes or
 CC primers, and in the recombinant production of a protein. The polypeptide
 CC are also useful in generating antibodies, as molecular weight markers,
 CC and as food supplements. The present sequence represents a specifically
 CC claimed human polypeptide sequence of the invention. Note: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format directly from WIPO at
 CC [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).
 XX SQ Sequence 145 AA;
 XX
 Query Match 84.1%; Score 645; DB 7; Length 145;
 Best Local Similarity 83.4%; Prod. No. 1.4e-62; Gaps
 Matches 121; Conservative 10; Mismatches 14; Indels 0; Gaps
 QY 1 MGCGGSRADAAIERYPIYESWTRTESTTWLYTSDALISAATNGSGPAGGLAGAVTGEDGP 60
 Db 1 MGCGGSRADAAIERYPIYESWTRTESTTWLYTSDALISAATNGSGPAGGLAGAVTGEDGP 60
 QY 61 SSGNVLRLPAPGSIANPERKKGCTQCNSNSLSSGSPITOKONGLWTEAKRDAKNSAR 12
 Db 61 PSNGVGPRASTAPGGIPNPERRKTCTEQCPNPOSLSLSSGPLTOKONGLWTEAKRDAKMPAK 12
 QY 121 EVAISITVENIQRDRSRVTKCIN 145
 Db 121 EYVINVVDISIQQMDRSRRTKNCVN 145
 RESULT 7
 ADM46959
 ID ADM46959 standard; protein: 145 AA.
 XX AC ADM46959;
 XX DT 03-JUN-2004 (first entry)
 XX DE Brain and Acute Leukemia, Cytoplasmic alternate protein #1.
 XX KW acute myelogenous leukemia; gene expression; BAALC;
 XX chronic myelogenous leukemia; prostate cancer; Brain and Acute Leukemia;
 XX Cytoplasmic; exon.
 OS Homo sapiens.
 XX PH Key Location/Qualifiers
 FT Misc-difference 41
 FT /note= "encoded by GCS"
 DN WO2003040347-A2.
 XX PD 15-MAY-2003.
 XX PP 12-NOV-2002; 2002WO-US036375.
 XX PR 09-NOV-2001; 2001US-0348210P.
 XX PA (OHIS) UNIV OHIO STATE RES FOUND.
 PT Tanner SM, De La Chapell A;
 XX DR N-PSDB; ADM46951.
 DR N-PSDB; ADM46951.
 XX PT Characterizing acute or chronic myelogenous leukemia, or prostate cancer
 CC in a patient comprises assaying for the overexpression of one or more
 CC BAALC transcripts in cells obtained from the patient, where an
 CC overexpression indicates that the patient has an aggressive form of AML.
 XX Disclosure; SEQ ID NO 17; 78PP; English.
 XX
 CC The invention relates to a method of characterizing acute myelogenous
 CC leukemia (AML) in a patient by assaying for the overexpression of one or
 CC more BAALC transcripts in cells obtained from the patient, where an
 CC overexpression indicates that the patient has an aggressive form of AML.
 XX Disclosure; SEQ ID NO 17; 78PP; English.

The methods, kits and probes are useful for characterizing acute or chronic myelogenous leukemia, or prostate cancer. They are also useful for detecting B-ALL overexpression. This sequence corresponds to a B-ALL (Brain and Acute Leukemia, Cytoplasmic) protein encoded by an alternative spliced RNA consisting of exons 1, 6 and 8.

CC screening agents for effectiveness in altering expression of the nucleic acid fragment; screening for agents useful for treating bone related disorders; evaluating the efficacy of a treatment of a bone related disorder in a subject; identifying polypeptides capable of binding to PAGB; monitoring the effectiveness of treatment of a subject with a bone related agent; a transgenic animal comprising the DNA; an animal model for the study of bone density modulation comprising a first group of animals composed of the transgenic animal and a second group of control animals; studying bone mass determinants; studying the modulation of bone mass; studying an effect of PAGB on bone disorders; identifying an agent for treating bone related disorders; identifying whether an agent which has bone forming activity; and a stably transfected cell line comprising two constructs, the first construct comprising a ligand binding domain linked to a DNA binding domain which is linked to an activation domain all of which expression is driven by a constitutive promoter, the second construct comprising multiple copies of DNA binding elements linked to a minimal promoter which is linked to PAGB cDNA, where upon the addition of chemical inducer, transcription of PAGB gene is induced. The PAGB polynucleotide has osteoplastic activity. The PTH responsive gene may be used to treat disorders by gene therapy. The nucleic acid is useful in preparing a composition for diagnosing, treating or preventing bone responsive gene protein of the invention.

XX SQ Sequence 145 AA;

Query Match Best Local Similarity 83.4%; Pred. No. 1-46-62; Length 145; Matches 121; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

Qy 1 MGCGGSRADAAIRPRYYESWTRTESTWLYTDSDALPSAATSGPENGGGLHAGVLEDP 60
1 MGCGGSRADAAIRPRYYESWTRTESTWLYTDSDALPSAATSGPENGGGLHAGVLEDP 60

Db 61 PSNCVPRSTAPGGIPNPEKKCTCOPCNPQSLSSGPLTQKONGLQTTEAKRDKRMSAR 120
61 PSNCVPRSTAPGGIPNPEKKCTCOPCNPQSLSSGPLTQKONGLQTTEAKRDKRMSAR 120

Qy 121 EVAISVTENIQMDRSKRVTNIN 145
121 EVAISVTENIQMDRSKRVTNIN 145

Db 121 EVTINVITSIQMDRSRITKCVN 145
121 EVTINVITSIQMDRSRITKCVN 145

RESULT 9
ADM46961 ID ADM46961 standard; protein; 180 AA.
AC ADM46961;
XX DT 03-JUN-2004 (first entry)
DE Brain and Acute Leukemia, Cytoplasmic alternate protein #3.
XX KW acute myelogenous leukemia; gene expression; BAALC;
KW chronic myelogenous leukemia; prostate cancer; Brain and Acute Leukemia; Cytoplasmic; exon.
XX OS Homo sapiens.
FH Key Location/Qualifiers
FT Misc-difference 41 /note= "encoded by GCS"
FT Misc-difference 41 /note= "encoded by GCS"
XX PN WO2003040347-A2.
XX PD 15-MAY-2003.
XX PR 12-NOV-2002; 2002WO-US036375.
XX PN 09-NOV-2001; 2001US-0348210P.
XX PA (OHIS) UNIV OHIO STATE RES FOUND.
XX DR WPI; 2003-441564/41.

PI Tanner SM, De La Chapell A;
XX DR WPT; 2003-441564/41.
N-PSDB; ADM46953.
XX PT Characterizing acute or chronic myelogenous Leukemia, or prostate cancer in a patient comprises assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient.
XX PT Disclosure; SEQ ID NO 19; 78pp; English.
The invention relates to a method of characterizing acute myelogenous Leukemia (AML) in a patient by assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient, where an overexpression indicates that the patient has an aggressive form of AML. The methods, kits and probes are useful for characterizing acute or chronic myelogenous leukemia, or prostate cancer. They are also useful for detecting BAALC overexpression. This sequence corresponds to a BAALC (Brain and Acute Leukemia, Cytoplasmic) protein encoded by an alternative spliced RNA consisting of exons 1, 6 and 8.
SQ Sequence 180 AA;
Query Match Best Local Similarity 67.2%; Pred. No. 2, 1e-59; Length 180; Matches 121; Conservative 10; Mismatches 14; Indels 35; Gaps 1;

Qy 1 MGCGGSRADAAIRPRYYESWTRTESTWLYTDSDALPSAATSGPENGGGLHAGVLEDP 60
1 MGCGGSRADAAIRPRYYESWTRTESTWLYTDSDALPSAATSGPENGGGLHAGVLEDP 60
Db 54 -----GVLEDGPSSNGVLRPAAGCIGANPEKKCT 85
Db 61 KIKAPRTSVSDEGLFSASKMPLAVFSGHGMLEDGLPSNGVRPSTAPGGIPNPEKKCT 120
Qy 86 QCPNSQSISSGGLTOKONGLWTTEAKRDKRMSAREVLTENIRQMDRSKRVTNIN 145
Db 121 QCPNQPSISSLGGPLTQKONGLQTTEAKRDKRMSRPAKEVTTINVDISIQMDRSRITKCVN 180

RESULT 10
ADM46963 ID ADM46963 standard; protein; 149 AA.
AC ADM46963;
XX DT 03-JUN-2004 (first entry)
DE Brain and Acute Leukemia, Cytoplasmic alternate protein #5.
XX KW acute myelogenous leukemia; gene expression; BAALC;
KW chronic myelogenous leukemia; prostate cancer; Brain and Acute Leukemia; Cytoplasmic; exon.
XX OS Homo sapiens.
FH Key Location/Qualifiers
FT Misc-difference 41 /note= "encoded by GCS"
XX PN WO2003040347-A2.
XX PD 15-MAY-2003.
XX PR 12-NOV-2002; 2002WO-US036375.
XX PR 09-NOV-2001; 2001US-0348210P.
XX PA (OHIS) UNIV OHIO STATE RES FOUND.
XX DR WPI; 2003-441564/41.

DR N-PSDB; ADO46955.

XX PT Characterizing acute or chronic myelogenous leukemia, or prostate cancer
 PT in a patient comprises assaying for the overexpression of one or more
 PT BIALC transcripts in cells obtained from the patient.
 XX PS Disclosure; SEQ ID NO 21; 78pp; English.

The invention relates to a method of characterizing acute myelogenous
 leukaemia (AML) in a patient by assaying for the overexpression of one or
 more BIALC transcripts in cells obtained from the patient, where an
 overexpression indicates that the patient has an aggressive form of AML.
 The methods, kits and probes are useful for characterizing acute or
 chronic myelogenous leukemia, or prostate cancer. They are also useful
 for detecting BIALC overexpression. This sequence corresponds to a BIALC
 (Brain and Acute Leukemia, Cytoplasmic) protein encoded by an alternative
 spliced RNA consisting of exons 1, 6 and 8.

XX SQ Sequence 149 AA;

Query Match 61.7%; Score 473.5; DB 7; Length 149;
 Best Local Similarity 66.0%; Pred. No. 1.2e-43; Matches 95; Conservative 2; Mismatches 12; Indels 35; Gaps 1;

QY 1 MGCGGSRADAEPRYYESWTRTESTWLTYDSDALPSAATDSGPBAGGHLA----- 53
 Db 1 MGCGGSRADAEPRYYESWTRTESTWLTYDSDALPSAATDSGPBAGGHLHSVLEAKS 60

QY 54 -----GVEDGGSSNGVTPAAMPGGTANPEKCONCCT 85
 Db 61 KIKAPTDVSDEGLPSASKMAPLAVFSGHMLEDGLPSNGYPRSTAGGIPNPEKKNCET 120

QY 86 QCPNSQSLSSGGPLTKONGJMTT 109
 Db 121 QCPNPFOSSLSSGGPLTKONGJQTT 144

RESULT 11
 ADQ81902
 ID ADO81902 Standard; protein; 92 AA.
 XX AC ADQ81902;
 XX DT 09-SEP-2004 (first entry)
 XX DE Human dioxygenase 10.12.
 XX KW Human; enzyme; dioxygenase 10.12; malignant tumour; inflammation;
 KW immunological disease; haemopathy; HIV infection.
 OS Homo sapiens.
 PN CN1347478-A.
 XX PD 17-APR-2002.
 XX PP 29-SEP-2000; 2000CN-00125495.
 XX PR 29-SEP-2000; 2000CN-00125495.
 XX PA (SHAN-) SHANGHAI BIODOR GENE DEV CO LTD.
 XX DR N-PSDB; ADO81901.

PT New nucleic acid fragment encoding a PAIGB polypeptide, useful in
 PT preparing a composition for diagnosing, treating or preventing bone
 PT related disorders, e.g., osteoporosis.

XX PS Claim 9; SEQ ID NO 10; 169pp; English.

XX The invention relates to a novel PTH responsive gene (PAIGB) fragment
 CC encoding a polypeptide. The invention further comprises: a chimeric
 CC construct comprising the isolated nucleic acid fragment operatively
 CC linked to suitable regulatory sequences; a host cell transformed with the
 CC chimeric construct; a vector comprising the nucleic acid fragment,
 CC obtaining a nucleic acid fragment encoding the polypeptide; a method for
 CC obtaining a polypeptide; detecting the presence of the nucleic acid
 CC fragment; an antibody that specifically binds to one or more epitopes of
 CC a PAIGB polypeptide; a composition for regulating bone-forming activity
 CC in a mammal comprising the nucleic acid fragment, polypeptide or antibody
 CC /, an agent that alters the expression of PAIGB gene or polypeptide mRNA;
 CC determining whether an agent alters the expression of PAIGB mRNA;

XX Claim 1; SEQ ID NO 2; 33pp; Chinese.

XX The present invention discloses a new kind of polypeptide, human
 CC dioxygenase 10.12, polynucleotides encoding this polypeptide, a DNA
 CC recombinant process to produce the polypeptide and antagonist against
 CC the polypeptide. The present invention also discloses the method of
 CC applying the polypeptide in treating various diseases, such as malignant
 CC tumours, inflammations, immunological diseases, haemopathy and HIV
 CC infection. The present sequence is the human dioxygenase 10.12.

XX SQ Sequence 92 AA;

Query Match 43.7%; Score 335.5; DB 5; Length 92;
 Best Local Similarity 72.7%; Pred. No. 1.1e-28; Matches 64; Conservative 9; Mismatches 10; Indels 5; Gaps 1;

QY 58 DGPSNGVTPAARGGIANPEKCONCCTCOPNSOSLISASPLTKONGJLWTEAKRDARM 117
 Db 10 DGPETGN----APGGIPNPEKKNCETQCPNPOSLISASPLTKONGJLWTEAKRDARM 64

QY 118 SAREVAISVTENIKOMDKRSKVTCIN 145
 Db 65 PAKEVNTIVDSDIQMDRSRRITKCNV 92

RESULT 12
 ADQ8481
 ID ADO8481 Standard; protein; 54 AA.
 XX AC ADQ8481;
 XX DT 12-AUG-2004 (first entry)
 XX DE Mouse PTH responsive gene protein exon 2 splice variant.
 XX KW PTH responsive gene; PAIGB; bone-forming; bone; bone density modulation;
 KW transgenic animal; osteopathic; gene therapy; osteoporosis; mouse;
 KW murine.
 XX OS Mus sp.
 XX PN WO2004044152-A2.
 XX PD 27-MAY-2004.
 XX PF 10-NOV-2003; 2003WO-US035655.
 XX PR 12-NOV-2002; 2002US-0425532P.
 XX PA (AMMP) WYETH.
 XX PI Robinson JA, Stojanovic-Sabulic V, Babij P, Murrills RJ;
 XX DR WPI; 2004-420299/39.
 XX DR N-PSDB; ADO8480.

PT New nucleic acid fragment encoding a PAIGB polypeptide, useful in
 PT preparing a composition for diagnosing, treating or preventing bone
 PT related disorders, e.g., osteoporosis.

XX PS Claim 9; SEQ ID NO 10; 169pp; English.

XX The invention relates to a novel PTH responsive gene (PAIGB) fragment
 CC encoding a polypeptide. The invention further comprises: a chimeric
 CC construct comprising the isolated nucleic acid fragment operatively
 CC linked to suitable regulatory sequences; a host cell transformed with the
 CC chimeric construct; a vector comprising the nucleic acid fragment,
 CC obtaining a nucleic acid fragment encoding the polypeptide; a method for
 CC obtaining a polypeptide; detecting the presence of the nucleic acid
 CC fragment; an antibody that specifically binds to one or more epitopes of
 CC a PAIGB polypeptide; a composition for regulating bone-forming activity
 CC in a mammal comprising the nucleic acid fragment, polypeptide or antibody
 CC /, an agent that alters the expression of PAIGB gene or polypeptide mRNA;
 CC determining whether an agent alters the expression of PAIGB mRNA;

CC spliced RNA consisting of exons 1, 6 and 8.
 CC
 XX Sequence 54 AA:
 SQ
 Query Match 36.2%; Score 278; DB 7; Length 54;
 CC Best Local Similarity 94.4%; Pred. No. 1.1e-22; Mismatches 2; Indels 0; Gaps 0;
 CC Matches 51; Conservative 1; Mismatches 2;
 QY 1 MGCGGSRADIAEPRYYESWRTETESTWLTTDSDALPSAATDSGPAGGLHAG 54
 Db 1 MGCGGSRADIAEPRYYESWRTETESTWLTTDSDALPSAATDSGPAGGLHAG 54

RESULT 15

ADD48477

ID ADD48477 standard; protein; 54 AA.

XX

AC ADD48477;

XX

DT 12-AUG-2004 (First entry)

XX

DE Human PTH responsive gene protein exon 2 splice variant.

XX

KW PTH responsive gene; PAIGB; bone forming; bone; bone density modulation; transgenic animal; osteopathic; gene therapy; osteoporosis; human.

XX

OS Homo sapiens.

XX

PN WO200404152-A2.

XX

PD 27-MAY-2004.

XX

PP 10-NOV-2003; 2003WO-US035655.

XX

PR 12-NOV-2002; 2002US-0425532P.

XX

PA (AMHP) WYETH.

XX

PT Robinson JA, Stojanovic-Subolic V, Babij P, Murrills RJ;

XX

DR N-FSDB; ADD48476.

XX

New nucleic acid fragment encoding a PAIGB polypeptide, useful in preparing a composition for diagnosing, treating or preventing bone related disorders, e.g., osteoporosis.

XX

Claim 9; SEQ ID NO 6; 169pp; English.

XX

The invention relates to a novel PTH responsive gene (PAIGB) fragment encoding a polypeptide. The invention further comprises: a chimeric construct comprising the isolated nucleic acid fragment operatively linked to suitable regulatory sequences; a host cell transformed with the chimeric construct; a vector comprising the nucleic acid fragment; obtaining a nucleic acid fragment encoding the polypeptide; a method for obtaining a polypeptide; detecting the presence of the nucleic acid fragment; an antibody that specifically binds to one or more epitopes of a PAIGB polypeptide; a composition for regulating bone-forming activity in a mammal comprising the nucleic acid fragment, polypeptide or antibody ; an agent that alters the expression of PAIGB gene or polypeptide; screening agents for effectiveness in altering expression of the nucleic acid fragment; screening for agents useful for treating bone related disorders; evaluating the efficacy of a treatment of a bone related disorder in a subject; identifying polypeptides capable of binding to PAIGB; monitoring the effectiveness of treatment of a subject with a bone related agent; a transgenic animal comprising the DNA; an animal model for the study of bone density modulation comprising a first group of animals composed of the transgenic animal and a second group of control animals; studying bone mass determinants; studying the modulation of bone mass; studying an effect of PAIGB on bone disorders; identifying an agent for treating bone related disorders; identifying whether an agent which has bone forming activity; and a stably transfected cell line comprising

CC two constructs, the first construct comprising a ligand binding domain linked to a DNA binding domain which is linked to an activation domain all of which expression is driven by a constitutive promoter, the second construct comprising multiple copies of DNA binding elements linked to a minimal promoter which is linked to PAIGB cDNA, where upon the addition of chemical inducer, transcription of PAIGB gene is induced. The PAIGB polymucleotide has osteopathic activity. The PTH responsive gene may be used to treat disorders by gene therapy. The nucleic acid is useful in preparing a composition for diagnosing, treating or preventing bone related disorders, e.g., osteoporosis. This sequence represents a PTH responsive gene protein of the invention.

SQ Sequence 54 AA;

Query Match 36.2%; Score 278; DB 8; Length 54;

CC Best Local Similarity 94.4%; Pred. No. 1.1e-22; Mismatches 2; Indels 0; Gaps 0;

CC Matches 51; Conservative 1; Mismatches 2;

QY 1 MGCGGSRADIAEPRYYESWRTETESTWLTTDSDALPSAATDSGPAGGLHAG 54

Db 1 MGCGGSRADIAEPRYYESWRTETESTWLTTDSDALPSAATDSGPAGGLHAG 54

Search completed: May 20, 2006, 20:18:06
Job time : 86 secs

;SEQ ID NO:4:
; LENGTH: 778
; 5198347-4

Query Match
Best Local Similarity 12.1%; Score 92.5; DB 7; Length 778;
Matches 29; Conservative 12; Mismatches 44; Indels 3; Gaps 3;

QY 31 TDSDALPSAATDSDGEPAGEGGIAGVAGLLEDGSSNGV-LRPAAPGGTANPERKKM-GTQP 88
Db 352 TYSVSPVSPVGKDSGPSTASAHALLAGENGWVHNGDTEPKEDGKADPQXDKIEVKGKDT 411

QY 89 NSQSLSS-GRTIQKONGLWTTEAKRDAK 115
Db 412 DDRSGCGSLGPHIDERTATLGTEHMEKDT 439

RESULT 3
US-09-328-352-8115
Sequence 8115, Application US/09328352
Patent No. 656258

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE REFERENCE: GTC9-03PA
CURRENT APPLICATION NUMBER: US/09/328, 352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 822
SEQ ID NO 8115
LENGTH: 726
TYPE: PRT
ORGANISM: Acinetobacter baumannii
US-09-328-352-8115

Query Match 11.0%; Score 84; DB 2; Length 726;
Best Local Similarity 35.1%; Pred. No. 1.2;
Matches 27; Conservative 8; Mismatches 22; Indels 20; Gaps 4;

QY 2 GCGGSSRADAAPEPRYYESWTRTESTWLTLYTDSDALPSA--ATPDSG----PEAGGLHAG 54
Db 181 GPGAGREDWVPDNVWNGDEK--WLAKRNSEALAGSNLAETMGLIVNPE----- 231

QY 55 VLGDPSSNGVLRPAP 71
Db 232 ---GPOASGDPRSAP 244

RESULT 4
US-09-408-647A-2
Sequence 2, Application US/09408647A
Patent No. 6399838

GENERAL INFORMATION:
APPLICANT: Kobayashi, Donald
TITLE OF INVENTION: Chitinase Gene from Stenotrophomonas
FILE REFERENCE: RUT-COOK 98-0020
CURRENT APPLICATION NUMBER: US/09/408, 647A
CURRENT FILING DATE: 1999-08-26
PRIOR APPLICATION NUMBER: 60/098, 036
PRIOR FILING DATE: 1998-08-27
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 700
TYPE: PRT
ORGANISM: Stenotrophomonas maltophilia

FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)..(41)
NAME/KEY: DOMAIN
LOCATION: (196)..(290)
NAME/KEY: DOMAIN

RESULT 5
US-09-408-647A-2
Sequence 60, Application US/094087558B
Patent No. 6949356

GENERAL INFORMATION:
APPLICANT: Bubby, Robert
APPLICANT: Cali, Brian
APPLICANT: Hecht, Peter
APPLICANT: Holtzman, Doug
APPLICANT: Madden, Kevin
APPLICANT: Maxon, Mary
APPLICANT: Milne, Todd
APPLICANT: No. 6949356an, Thea
APPLICANT: Royer, John
APPLICANT: Salama, Sofie
APPLICANT: Sherman, Amir
APPLICANT: Silva, Jeff
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 10272-130
CURRENT APPLICATION NUMBER: US/09/487, 558B
CURRENT FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/487, 558
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 446
SEQ ID NO: Patentin version 3.0
LENGTH: 60
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-09-407-550B-60

Query Match 10.9%; Score 83; DB 2; Length 1433;
Best Local Similarity 29.4%; Pred. No. 4.4;
Matches 32; Conservative 15; Mismatches 50; Indels 12; Gaps 4;

QY 36 LPSAATTSGPEAGGLHAGVLEGPSSNGVLRPAPGGTANPERKKM-GTQP 95
Db 927 LPPATTTSKPLFGQSQNSLNRLNRTPNKR-----ENPEHEVLYGNDNNNNSEA 979

QY 96 G--PLTQKONGLWTTEAKRDAKMSARSAVIASTENIR-QMRSKRT 140
Db 980 GHSMINTTNGNKLKVKDKE-NAKQGIGSKGENANFQNTKOMS 1027

RESULT 6
US-09-071-035-176
Sequence 176, Application US/09071035
Patent No. 6448043

GENERAL INFORMATION:

APPLICANT: Gil H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUNENCES: 496

OPERATING SYSTEM: Windows 98
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
A D D Y C O M P U T E R S , I C / 1 / 2 0 0 1

APPLICATION NUMBER: US/10/2006/316
FILING DATE: 29-JUL-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/071,035

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage

CONTROLLER: NM VECTRA 486/33
OPERATING SYSTEM: MSDOS version 6.
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: IIS/09/071 035

LAW OFFICES OF
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:

FILING DATE: **ATTORNEY/AGENT INFORMATION:**
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373

REFERENCE/DOCKET NUMBER: PB356
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SRO ID NO: 176

SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: protein
9-071-035-176

3 CGG-----SRADATEPRYVEE
 Match 10.4%; Score 10.4%;
 st Local Similarity 26.6%; Pre-
 tches 47; Conservative 16; In-

1 CGGGKSTENTDSRSSAAESTVESTKASATKESSSK-ATTKSSDAKPSGTTPADSKATAS
5' GLHAGVJEDGPPSSNGVLPAPGGIANPEKKRN-CGTTQCPN--S9S1S8S3L7TQKONGL

60 STKEA-----ANNSAEIKOSPAQANPDDQANQVLNQLANMPFCGGLPQALITSQTNNF 113
106 WTEAKRDAKRMSSAREVAISVTENTIROMI-RSKRT-----KNCIN 145

T 7
114 LTAAATSOQADQNPRVLYYEAEKEAIPVNDAVNQLOPISSEFEKKTYGSDEAKNAV 170

-206-576-176
quence 176, Application US/10206576
ent No. 6913907
GENERAL INFORMATION:

APPLICANT: Choi et al.
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 497
CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences
STREET: 9410 West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA

ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: Dell Latitude

ATTORNEY/AGENT INFORMATION:

NAME: A. Anders Brookes

REGISTRATION NUMBER: 36,373

REFERENCE/DOCKET NUMBER: PB369P2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8512

TELEFAX: (301) 309-8504

INFORMATION FOR SEQ ID NO: 174:

SEQUENCE CHARACTERISTICS:

LENGTH: 305 amino acids

TYPE: amino acid

STRANDBEDNESS: Single

MOLECULE TYPE: protein

US-09-071-035-174

Query Match 10.4%; Score 79.5; DB 2; Length 305;
 Best Local Similarity 26.6%; Pred. No. 1.2; Mismatches 73; Indels 41; Gaps 9;
 Matches 47; Conservative 16; MisMatches 73; Indels 41; Gaps 9;

QY 3 CGG-----SRAADEIPRYYESW---TRETESTWLTYTDSDALPSAAT-DSGPEAG 49
 Db 20 CGGGKSTENTDRSSAAESTTVESTKASATKESSK-ATTKSSAKPSCTTADSKATAS 78

QY 50 GLHAGVILEDGPPSSNGVLRPAPGGIANPDKMN-CGTCOPN--SOSLSSGPLOTOKONGL 105
 Db 79 STKEA-----ANNSAEKQSPAKMANPDDQANQVNQLANMFPQGQGLPQALTSQTNF 132

QY 106 WTTEAKRDAKMSAREVAISVTENIRQMD-RSKRVT-----KNCIN 145
 Db 133 LTATTSDAQDNFRVLYYAEKEAIPVNDARVNOLTPISSFEKRTYGSDAEAKNAVN 189

RESULT 10

US-10-076-622-552

Sequence 552, Application US/10076622

; Patent No. 6958361

; GENERAL INFORMATION:

; APPLICANT: Houghton, Raymond L.

; APPLICANT: Sleath, Paul R.

; APPLICANT: Persing, David H.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER

; CURRENT APPLICATION NUMBER: US/10/076,622

; FILE REFERENCE: 210121.470C1

; CURRENT FILING DATE: 2002-02-13

; NUMBER OF SEQ ID NOS: 627

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 552

; LENGTH: 661

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-076-622-552

Query Match 10.4%; Score 79.5; DB 2; Length 661;
 Best Local Similarity 21.5%; Pred. No. 3.6; Mismatches 37; Indels 58; Gaps 7;
 Matches 37; Conservative 28; MisMatches 58; Indels 49; Gaps 7;

QY 7 RADAEIP----RYYESWRETESTWLTYTDSD-ALPSAATDSGPEAGVLLGAGVLECP 60
 Db 401 RADILPESKSKDYEBSWSDSLCETVSQDVCLPKRAHOKEIDKIN---GKLEESP 456

QY 61 SSGVVRRAAPGGIANPDKMN-CGTCOPN--SOSLSSGPLOTOKONGL 90
 Db 457 DNGFLPLSPCRMVKSYIPTKALEMDOPTPKASPEKPSAFPAIEMOKSPVNPALKELNE 516

QY 91 QSISSG----PLTOKONGL---WTTEAKRDAKMSAREVAISVTENIRQMDR 135
 Db 517 QTLDADWPSKSKQKONVENSIDSSERET-VSQDVCVPATHQEMDK 566

RESULT 11

US-10-124-805-552

; Sequence 552, Application US/1012405

; GENERAL INFORMATION:

; APPLICANT: Houghton, Raymond L.

; APPLICANT: Sleath, Paul R.

; APPLICANT: Persing, David H.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER

; FILE REFERENCE: 210121.470C12

RESULT 9

Sequence 174, Application US/10206576

Patent No. 6913907

GENERAL INFORMATION:

APPLICANT: Choi et al.

TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides

NUMBER OF SEQUENCES: 497

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-R

COMPUTER: Dell Latitude

OPERATING SYSTEM: Windows 98

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/206,576

FILING DATE: 29-JUL-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/071,035

FILING DATE: 1998-05-04

APPLICATION NUMBER: US 60/046,655

FILING DATE: 1997-05-16

APPLICATION NUMBER: US 60/044,031

FILING DATE: 1997-05-06

APPLICATION NUMBER: US 60/066,009

FILING DATE: 1997-11-14

ATTORNEY/AGENT INFORMATION:

NAME: Human, Mark J.

REGISTRATION NUMBER: 46,789

REFERENCE/DOCKET NUMBER: PB369P1D1

INFORMATION FOR SEQ ID NO: 174:

SEQUENCE CHARACTERISTICS:

LENGTH: 305 amino acids

RESULT 13
US-10-124-805-553
; SEQUENCE 553, Application US/10124805
; PATENT NO. 695918
; GENERAL INFORMATION:
; APPLICANT: Houghton, Raymond L.
; TYPE: PRT
; ORGANISM: Homo sapiens

RESULT 12
US-10-076-622-553
; Sequence 553, Application US/10076622
; Patent No. 6958361
; GENERAL INFORMATION:
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSTICS OF BREAST CANCER
; FILE REFERENCE: 210121-47011
; CURRENT APPLICATION NUMBER: US/10/076,622
; CURRENT FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 627
; SOFTWARE: FASTSEQ FOR Windows Version 4.0
; SEQ ID NO 553
; LENGTH: 1013
; TYPE: PRT
; ORGANISM: Homo sapiens

RESULT 14
US-08-374-077C-2
; Sequence 2, Application US/08374077C
; Patent No. 6027912
; GENERAL INFORMATION:
; APPLICANT: Hall, Linda M.
; APPLICANT: Ren, Dejian
; APPLICANT: Zheng, Wei
; APPLICANT: Dubald, Manuel Marcel Paul
; TITLE OF INVENTION: Genes Encoding an Invertebrate Alpha1
; TITLE OF INVENTION: Calcium Channel Subunit
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314-3187
; COMPUTER READABLE FORM:
; COMPUTER: FLOPPY disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/374,077C
; FILING DATE: 19-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McGowan, Malcolm M.
; REGISTRATION NUMBER: 39,300
; REFERENCE/DOCKET NUMBER: 022650-264
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-835-2021
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2516 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-374-077C-2

Query Match 10.2%; Score 78.5; DB 2; Length 2516;
 Best Local Similarity 22.4%; Pred. No. 33; Mismatches 21; Indels 53; Gaps 8;
 Matches 39; Conservative 21; Mismatches 61; Indels 53; Gaps 8;

Qy 3 CGGSRADATEPRY--YESWTRERESTWLTYTDSDALPSAATSGPENAGGLAHAGVLEDGP 60
 Db 207 CGGGCGISAPPRLPEEAMQLQPQ-----NSVTAGSTNSFSSGG-----GR 249

Qy 61 SNGVLRPAPGGIANPEKGNC-----GRQC-----PNS 90
 Db 250 DDNSYY--SAVGGSSSSNCSNCITGDNSTLHGLGVGVCFSFTADCDNSEDDDGDPN 307

Qy 91 QSLSSGPL-TOKQNLWTTEAKRDAKMSAREVAISVTENIRQMDRSKRVTNC 143
 Db 308 QDLSQRTARTAIVAAVAAKEOQEQSLADE-SFSDRRQDADEDVRIODC 360

RESULT 15
 US-08-895-590-2
 ; Sequence 2, Application US/08895590
 ; Patent No. 6207410
 ; GENERAL INFORMATION:
 ; APPLICANT: Hall, Linda M.
 ; APPLICANT: Ren, Bejian
 ; APPLICANT: Zheng, Wei
 ; APPLICANT: Dubald, Manuel Marcel Paul
 ; TITLE OF INVENTION: Genes Encoding an Insect Calcium Channel
 ; NUMBER OF SEQUENCES: 101
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BURNS, DOANE, SWCKER & MATHEIS, LLP
 ; STREET: 699 Prince Street
 ; CITY: Alexandria
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22314-3187
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/895,590
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: McDowall, Malcolm M.
 ; REGISTRATION NUMBER: 39,300
 ; REFERENCE/DOCKET NUMBER: 022650-263
 ; TELECOMMUNICATION INFORMATION:
 ; TELEFAX: 703-336-2021
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2516 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-895-590-2

Query Match 10.2%; Score 78.5; DB 2; Length 2516;
 Best Local Similarity 22.4%; Pred. No. 33; Mismatches 21; Indels 53; Gaps 8;
 Matches 39; Conservative 21; Mismatches 61; Indels 53; Gaps 8;

Qy 3 CGGSRADATEPRY--YESWTRERESTWLTYTDSDALPSAATSGPENAGGLAHAGVLEDGP 60
 Db 207 CGGGCGISAPPRLPEEAMQLQPQ-----NSVTAGSTNSFSSGG-----GR 249

Qy 61 SNGVLRPAPGGIANPEKGNC-----GRQC-----PNS 90
 Db 250 DDNSYY--SAVGGSSSSNCSNCITGDNSTLHGLGVGVCFSFTADCDNSEDDDGDPN 307

Qy 91 QSLSSGPL-TOKQNLWTTEAKRDAKMSAREVAISVTENIRQMDRSKRVTNC 143
 Db 308 QDLSQRTARTAIVAAVAAKEOQEQSLADE-SFSDRRQDADEDVRIODC 360

Search completed: May 20, 2006, 21:21:21
 Job time : 52 secB

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 20, 2006, 21:21:43 ; Search time 74 Seconds
 (Without alignments)

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published Applications Ax Main:
 1: /EMC_Celerra_SIDS3/ptodata/2/pupaa/us07_PUBCOMB.pep: *
 2: /EMC_Celerra_SIDS3/ptodata/2/pupaa/us09_PUBCOMB.pep: *
 3: /EMC_Celerra_SIDS3/ptodata/2/pupaa/us10_PUBCOMB.pep: *
 4: /EMC_Celerra_SIDS3/ptodata/2/pupaa/us10_PUBCOMB.pep: *
 5: /EMC_Celerra_SIDS3/ptodata/2/pupaa/us11_PUBCOMB.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

§ SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	767	100.0	145	4 US-10-705-716A-2
2	746	97.3	145	4 US-10-705-716A-8
3	645	84.1	145	4 US-10-233-233-17
4	645	84.1	145	4 US-10-177-390-30
5	617.5	80.5	145	4 US-10-705-716A-4
6	617.5	80.5	180	4 US-10-233-233-19
7	473.5	61.7	149	4 US-10-233-233-21
8	294	38.3	54	4 US-10-705-716A-10
9	288	37.5	73	4 US-10-293-233-20
10	278	36.2	54	4 US-10-233-233-18
11	278	36.2	54	4 US-10-705-716A-6
12	272	35.5	80	4 US-10-233-233-22
13	140	18.3	25	4 US-10-893-233-37
14	99	12.9	18	4 US-10-233-233-35
15	94	12.7	147	4 US-10-705-716A-10
16	93	12.1	394	4 US-10-25-115-236244
17	89	11.6	16	4 US-10-705-716A-11
18	87.5	11.4	260	5 US-10-450-763-49566
19	87.5	11.4	592	5 US-10-450-763-49566
20	85.5	11.1	264	4 US-10-425-115-275422
21	85.5	11.1	274	4 US-10-425-114-65588
22	85	11.1	450	4 US-10-437-963-137075
23	84	11.0	718	4 US-10-282-1224-42268
24	83	10.8	1433	3 US-09-801-368-60
25	83	10.8	1433	4 US-10-449-310-112
26	82.5	10.8	514	6 US-11-188-289-18211
27	82.5	10.8	US-10-424-599-227399	4 US-10-424-599-227399

§ ALIGNMENTS

RESULT 1
 US-10-705-716A-2

; Sequence 2, Application US/10705716A
 ; Publication No. US20040146906A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Robinson, John Allen
 ; APPLICANT: Stojanovic-Susulic, Vedrana
 ; APPLICANT: Babić, Philip
 ; APPLICANT: Murillis, Richard John
 ; TITLE OF INVENTION: A Novel PTH Responsive Gene
 ; FILE REFERENCE: AML00401
 ; CURRENT APPLICATION NUMBER: US/10/705-716A
 ; CURRENT FILING DATE: 2003-11-10
 ; PRIOR APPLICATION NUMBER: US 60/425,532
 ; PRIORITY FILING DATE: 2002-11-12
 ; NUMBER OF SEQ ID NOS: 63
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 2
 ; LENGTH: 145
 ; TYPE: PRT
 ; ORGANISM: Rat

US-10-705-716A-2

Query Match Best Local Similarity 100.0%; Score 767; DB 4; Length 145;
 Matches 145, Conservative 0, Mismatches 0, Indels 0; Gaps 0;

Qy 1 MGCGGSRADATEPRYTESWRETESTSWTLYTDSDALPSAATDSGSEAGGLAHAVLGDGP 60
 Db 1 MGCGGSRADATEPRYTESWRETESTSWTLYTDSDALPSAATDSGSEAGGLAHAVLGDGP 60

Qy 61 SSNGVLRPAAPGGIANPKKNGCTQCPNSOSSPLQTOKONGLWTEAKRDAKMSR 120
 Db 61 SSNGVLRPAAPGGIANPKKNGCTQCPNSOSSPLQTOKONGLWTEAKRDAKMSR 120

Qy 121 EVAISIENRQMDISKRVTKNCIN 145
 Db 121 EVAISIENRQMDISKRVTKNCIN 145

RESULT 2
 US-10-705-716A-8

; Sequence 8, Application US/10705716A
 ; Publication No. US20040146906A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Robinson, John Allen
 ; APPLICANT: Stojanovic-Susulic, Vedrana
 ; APPLICANT: Babić, Philip
 ; APPLICANT: Murillis, Richard John
 ; TITLE OF INVENTION: A Novel PTH Responsive Gene

FILE REFERENCE: AML00401
; CURRENT APPLICATION NUMBER: US/10/705,716A
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: US 60/425,532
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 8
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Mouse
; US-10-705-716A-8

Query Match
; Best Local Similarity 97.3%; Score 746; DB 4; Length 145;
; Matches 141; Conservative 97.2%; Pred. No. 7, 1e-67; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MCGGGRADAEPRYYESTWTTYTDALPSAAADSGPAGGLAHAGVLDGP 60
; 1 MSGGGSRDAEPRYYESTWTTYTDALPSAAADSGPAGGLAHAGVLDGL 60

Db 61 SSGNGVLRPAAPGIANPEKKONGTQCPNSQNSLSSGSPLTOKONGLWTEAKDAKRSAR 120
; 61 SSGNGVLRPAAPGIANPEKKONGTQCPNSQNSLSSGSPLTOKONGLWTEAKDAKRSAR 120

Qy 121 EVAISVTENIRQMDRSKRVTNCIN 145
; 121 EVAISVTENIRQMDRSKRVTNCIN 145

Db 121 EVAINVTENIRQMDRSKRVTNCIN 145
; 121 EVAINVTENIRQMDRSKRVTNCIN 145

RESULT 3
US-10-293-239-17
; Sequence 17, Application US/10293239
; Publication No. US200319043A1
; GENERAL INFORMATION:
; APPLICANT: Tanner, Stephan
; TITLE OF INVENTION: BALTIC expression as a diagnostic marker for acute leukemia
; FILE REFERENCE: 2272/0101
; CURRENT APPLICATION NUMBER: US/10/293, 239
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 60/318, 210
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 17
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-293-239-17

Query Match
; Best Local Similarity 84.1%; Score 645; DB 4; Length 145;
; Matches 121; Conservative 83.4%; Pred. No. 1e-56; Mismatches 10; Indels 0; Gaps 0;

Qy 1 MCGGGRADAEPRYYESTWTTYTDALPSAAADSGPAGGLAHAGVLDGP 60
; 1 MCGGGRADAEPRYYESTWTTYTDALPSAAADSGPAGGLAHAGVLDGL 60

Db 61 SSGNGVLRPAAPGIANPEKKONGTQCPNSQNSLSSGSPLTOKONGLWTEAKDAKRSAR 120
; 61 SSGNGVLRPAAPGIANPEKKONGTQCPNSQNSLSSGSPLTOKONGLWTEAKDAKRSAR 120

Qy 121 EVAISVTENIRQMDRSKRVTNCIN 145
; 121 EVAISVTENIRQMDRSKRVTNCIN 145

Db 121 EVAISVTENIRQMDRSKRVTNCIN 145
; 121 EVAISVTENIRQMDRSKRVTNCIN 145

RESULT 5
US-10-705-716A-4
; Sequence 4, Application US/10705716A
; Publication No. US2004014696A1
; GENERAL INFORMATION:
; APPLICANT: Robinson, John Allen
; APPLICANT: Stojanovic-Susolic, Vedrana
; APPLICANT: Babij, Philip
; APPLICANT: Murrills, Richard John
; TITLE OF INVENTION: A Novel PTH Responsive Gene
; FILE REFERENCE: AML00401
; CURRENT APPLICATION NUMBER: US/10/705,716A
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: US 60/425,532
; PRIOR FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 4
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-705-716A-4

Query Match
; Best Local Similarity 84.1%; Score 645; DB 4; Length 145;
; Matches 121; Conservative 83.4%; Pred. No. 1e-56; Mismatches 10; Indels 0; Gaps 0;

Qy 1 MCGGGRADAEPRYYESTWTTYTDALPSAAADSGPAGGLAHAGVLDGP 60
; 1 MCGGGRADAEPRYYESTWTTYTDALPSAAADSGPAGGLAHAGVLDGL 60

Db 61 SSGNGVLRPAAPGIANPEKKONGTQCPNSQNSLSSGSPLTOKONGLWTEAKDAKRSAR 120
; 61 SSGNGVLRPAAPGIANPEKKONGTQCPNSQNSLSSGSPLTOKONGLWTEAKDAKRSAR 120

Qy 121 EVAISVTENIRQMDRSKRVTNCIN 145
; 121 EVAISVTENIRQMDRSKRVTNCIN 145

Db 121 EVAISVTENIRQMDRSKRVTNCIN 145
; 121 EVAISVTENIRQMDRSKRVTNCIN 145

RESULT 4
US-10-177-390-30
; Sequence 30, Application US/0177390
; Publication No. US2003014374A1
; GENERAL INFORMATION:

RESULT 6

US-10-293-239-19
; Sequence 19, Application US/10293239
; Publication No. US20030119043A1
; GENERAL INFORMATION:
; APPLICANT: de la Chapelle, Albert
; TITLE OF INVENTION: B41C expression as a diagnostic marker for acute leukemia
; FILE REFERENCE: 22727/04101
; CURRENT APPLICATION NUMBER: US/10/293,239
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: US 60/348,210
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-293-239-19
Query Match 80.5%; Score 617.5; DB 4; Length 180;
Best Local Similarity 67.2%; Pred. No. 8.1e-54;
Matches 121; Conservative 10; Mismatches 14; Indels 35; Gaps 1;
Qy 1 MGCGGSRADAEIPTYVYESWTRTESTWLTYTSDALPSAAATSGPEAGGLHA----- 53
Db 1 MGCGGSRADAEIPTYVYESWTRTESTWLTYTSDALPSAAATSGPEAGGLHSLEAKS 60
Qy 54 -----GVIEDGPSSNGVLRPAPPGIANPKKONGT 85
Db 61 KIKAPTDVSDEGLFSASKNMAPLAVFSHGMLEDGLPSNCVPRTAPGGIPNPPEKTNCT 120
Qy 86 QCPNSQSLSSGPLTOKONGWTEAKRDAKRMGSAREVALSVTENIRONDRSKRVTKGNCN 145
Db 121 QCNPQPSLSSGPLTOKONGLQTTEAKRDAKRMPSAKEVTINVTISIQMDRSRRTKCN 180
RESULT 7
US-10-293-239-21
; Sequence 21, Application US/10293239
; Publication No. US20030119043A1
; GENERAL INFORMATION:
; APPLICANT: Tanner, Stephan
; TITLE OF INVENTION: B41C expression as a diagnostic marker for acute leukemia
; FILE REFERENCE: 22727/04101
; CURRENT APPLICATION NUMBER: US/10/293,239
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 60/348,210
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-293-239-21
Query Match 61.7%; Score 473.5; DB 4; Length 149;
Best Local Similarity 66.0%; Pred. No. 2e-39; Mismatches 12; Indels 35; Gaps 1;
Matches 95; Conservative 2; Mismatches 12; Indels 35; Gaps 1;
Qy 1 MGCGGSRADAEIPTYVYESWTRTESTWLTYTSDALPSAAATSGPEAGGLHA----- 53
Db 1 MGCGGSRADAEIPTYVYESWTRTESTWLTYTSDALPSAAATSGPEAGGLHSLEAKS 60
Qy 54 -----GVLEDGPSSNGVLRPAPGGIANPKKONGT 85
Db 61 KIKAPTDVSDEGLFSASKNMAPLAVFSHGMLEDGLPSNCVPRTAPGGIPNPPEKTNCT 120
Qy 86 QCPNSQSLSSGPLTOKONGWTE 109
Db 121 QCNPQPSLSSGPLTOKONGLQTIE 144
RESULT 8
US-10-705-716A-10
; Sequence 10, Application US/10705716A
; Publication No. US20040146906A1
; GENERAL INFORMATION:
; APPLICANT: Robinson, John Allen
; APPLICANT: Stojanovic-Subotic, Vedrana
; APPLICANT: Babilj, Philip
; APPLICANT: Murillis, Richard John
; TITLE OF INVENTION: A Novel PRM Responsive Gene
; FILE REFERENCE: AM100401
; CURRENT APPLICATION NUMBER: US/10/705,716A
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: US 60/425,532
; PRIOR FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Mouse
; US-10-705-716A-10
Query Match 38.3%; Score 294; DB 4; Length 54;
Best Local Similarity 100.0%; Pred. No. 6.6e-22;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGCGGSRADAEIPTYVYESWTRTESTWLTYTSDALPSAAATSGPEAGLHAG 54
Db 1 MGCGGSRADAEIPTYVYESWTRTESTWLTYTSDALPSAAATSGPEAGLHAG 54
RESULT 9
US-10-293-239-20
; Sequence 20, Application US/10293239
; Publication No. US20030119043A1
; GENERAL INFORMATION:
; APPLICANT: Tanner, Stephan
; TITLE OF INVENTION: B41C expression as a diagnostic marker for acute leukemia
; FILE REFERENCE: 22727/04101
; CURRENT APPLICATION NUMBER: US/10/293,239
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 60/348,210
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-293-239-20
Query Match 37.5%; Score 288; DB 4; Length 73;
Best Local Similarity 91.4%; Pred. No. 3.9e-21;
Matches 53; Conservative 2; Mismatches 21; Indels 0; Gaps 0;
Qy 1 MGCGGSRADAEIPTYVYESWTRTESTWLTYTSDALPSAAATSGPEAGGLHAGVLD 58
Db 1 MGCGGSRADAEIPTYVYESWTRTESTWLTYTSDALPSAAATSGPEAGGLHSGLCIE 58
RESULT 10
US-10-293-239-18
; Sequence 18, Application US/10293239
; Publication No. US20030119043A1
; GENERAL INFORMATION:
; APPLICANT: Tanner, Stephan
; APPLICANT: de la Chapelle, Albert
; TITLE OF INVENTION: B41C expression as a diagnostic marker for acute leukemia
; FILE REFERENCE: 22727/04101

; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21 (53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 6128
; SEQ ID NO 48905
; LENGTH: 147
; TYPE: PRT
; FEATURE:
; ORGANISM: Sorghum bicolor
; OTHER INFORMATION: Clone ID: LIB3476-020-PI-K1-A12.pep
US-10-767-701-48905

Query Match 12.3%; Score 94; DB 4; Length 147;
Best Local Similarity 27.5%; Pred. No. 0.32; Gaps 3;
Matches 30; Conservative 17; Mismatches 52; Indels 10; Gaps 3;
Qy 36 LPSIAATSGPAGGLHAGVLEDDPSSNGVLRPAPGIANPKRMANCTCNSQS-- 92
Db 29 LPALALPDAEAGLAGDNGGAGHGPGRG--QAEAGAGARQALHCOPCPFHSDSCIG 84
Qy 93 -LSSGPLTOKO-NGLWTTTEAKDADKMSAREVAISVTENIROMDRSKR 138
Db 85 RWISIGTSGHRPCSGLLSVQLRQMPRSSAAQVKREIKKQIQEQRVRR 133

Search completed: May 20, 2006, 21:23:19
Job time : 75 secs

GenCore version 5.1.8
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OM protein - protein search, using bw model

Run on:

May 20, 2006, 21:23:34 ; Search time 5 Seconds

(without alignments)
61.947 Million cell updates/sec

Title: US-10-705-716a-2

Perfect score: 767

Sequence: 1 MGCGSRADAIEPRVYRSWT.....VTENIQRDRSKRVTNCIN 145

Scoring table: BLASTM62

Gapop 10.0 , Gapext 0.5

Searched: 21570 seqs, 2136119 residues

Total number of hits satisfying chosen parameters: 21570

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Database : Published Applications As New,*

1: /EMC_Celerra_SINS3/prodata/2/pupbaa/US09_NEW_PUB_pep:*

2: /EMC_Celerra_SINS3/prodata/2/pupbaa/US06_NEW_PUB_pep:*

3: /EMC_Celerra_SINS3/prodata/2/pupbaa/US07_NEW_PUB_pep:*

4: /EMC_Celerra_SINS3/prodata/2/pupbaa/US08_NEW_PUB_pep:*

5: /EMC_Celerra_SINS3/prodata/2/pupbaa/PCT_NEW_PUB_pep:*

6: /EMC_Celerra_SINS3/prodata/2/pupbaa/US10_NEW_PUB_pep:*

7: /EMC_Celerra_SINS3/prodata/2/pupbaa/US11_NEW_PUB_pep:*

8: /EMC_Celerra_SINS3/prodata/2/pupbaa/US60_NEW_PUB_pep:*

Pred. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Length DB ID Description

Result No.	Score	Query	Length	DB	ID	Description
1	64.5	8.4	356	6	US-10-505-928-391	Sequence 391, App
2	64.5	8.4	413	6	US-10-511-937-2428	Sequence 2428, App
3	64	8.3	262	6	US-10-370-959-131	Sequence 131, App
4	64	8.3	474	6	US-11-301-559-1812	Sequence 1812, App
5	63.5	8.3	443	6	US-10-511-937-2464	Sequence 2464, App
6	62	8.1	2671	6	US-10-505-928-784	Sequence 784, App
7	61.5	8.0	404	7	US-11-251-465-23	Sequence 23, App
8	61.5	8.0	1075	6	US-10-322-835-48	Sequence 48, App
9	60.5	7.9	353	6	US-10-0-924-851	Sequence 851, App
10	60	7.8	428	6	US-10-196-749-514	Sequence 514, App
11	59.5	7.8	734	6	US-10-196-749-458	Sequence 458, App
12	59	7.7	702	6	US-10-0-38-636	Sequence 363, App
13	59	7.7	2026	6	US-10-05-928-831	Sequence 831, App
14	58.5	7.6	663	7	US-11-169-140-14	Sequence 14, App
15	58.5	7.6	4590	6	US-10-505-928-569	Sequence 569, App
16	56.5	7.6	564	6	US-10-511-937-2557	Sequence 2557, App
17	58	7.6	730	6	US-10-0-505-928-841	Sequence 841, App
18	57.6	7.6	1645	6	US-10-505-928-582	Sequence 582, App
19	58	7.6	2413	6	US-10-511-937-2616	Sequence 2616, App
20	57.5	7.5	980	7	US-11-242-505A-36	Sequence 36, App
21	57	7.4	635	6	US-10-511-937-2424	Sequence 2424, App
22	57	7.4	720	7	US-10-0-928-383	Sequence 383, App
23	56.5	7.4	400	7	US-11-183-218-46	Sequence 46, App
24	56.5	7.4	558	7	US-11-311-759-31	Sequence 31, App
25	56.5	7.4	678	6	US-10-196-749-150	Sequence 150, App

ALIGNMENTS

RESULT 1
US-10-505-928-391

; Sequence 391, Application US/10505928

; Publication No. US20060088532A1
; GENERAL INFORMATION:

; APPLICANT: Ludwig Institute for Cancer Research et al.

; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES

; FILE REFERENCE: 28967/39178

; CURRENT APPLICATION NUMBER: US/10-505-928

; CURRENT FILING DATE: 2004-08-27

; PRIORITY APPLICATION NUMBER: US 60/363,391

; NUMBER OF SEQ ID NOS: 866

; SOFTWARE: Patentin 3.2

; SEQ ID NO: 391

; LENGTH: 356

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-505-928-391

Query Match Similarity 8.4%; Score 64.5; DB 6; Length 356;
Best Local Similarity 35.8%; Pred. No. 5.1; Mismatches 17; Indels 9; Gaps 4;

Matches 19; Conservative 35.8%; Pred. No. 5.1; Mismatches 17; Indels 9; Gaps 4;

Qy 60 PSSNGGLRPAAPGGTANPDKKNCNGTQCQPNQSLSGGP--ITQKONGLWTERA 110

Db 225 PDLPGVLPAPDPG--PPEER--GEHSRSPSPVGRGPQVTSMSSWQCA 270

; GENERAL INFORMATION:

; APPLICANT: EXPRESSION DIAGNOSTICS, INC.

; APPLICANT: Wohlgemuth, Jay

; APPLICANT: Fry, Kirk

; APPLICANT: Woodward, Robert

; APPLICANT: LY, Ngoc

; APPLICANT: Prentice, James

; APPLICANT: Morris, MacDonald

; APPLICANT: Rosenberg, Steven

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING

; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION

; FILE REFERENCE: 506612000104

; CURRENT APPLICATION NUMBER: US/10-511,937

; CURRENT FILING DATE: 2004-10-19

; PRIOR APPLICATION NUMBER: PCT/US2003/012946

PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 2428
; LENGTH: 413
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-511-937-2428

Query Match 8.4%; Score 64.5; DB 6; Length 413;
; Best Local Similarity 24.2%; Pred. No. 6.3; Mismatches 23;保守性 Matches 12; Indels 35; Gaps 4;

Qy 63 NGSVLRPAPPGGANPEKDN--NCGTQCPNSQSL-----SSG----- 96
Db 235 NCQNRP---LIRPKKGILIVSGRAGQCTNQTTTLMRNNSGDPVCNAAGLYKLH 289

RESULT 3 US-10-370-959-131

; Sequence 131, Application US/10370959
; Publication No. US20060088907A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Meyers, Rachael E.
; APPLICANT: Williamson, Mark W.
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: MacBeth, Kylie J.
; APPLICANT: Hunter, John J.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Bandaru, Rajasekhar
; APPLICANT: Tsai, Fong-Ying
TITLE OF INVENTION: NOVEL 1237, 18480, 2245, 16228, 7677, TITLE OF INVENTION: 24320, 46619, 33166, 16836, 46807, 21617, 55562, 39228, TITLE OF INVENTION: 62088, 46745, 23155, 16836, 46807, 21617, 55562, 39228, AND TITLE OF INVENTION: 3225. MOLECULES AND USES THEREFOR FILE REFERENCE: MP103-017OMNM CURRENT APPLICATION NUMBER: US/10/370,959 CURRENT FILING DATE: 2003-02-20 PRIOR APPLICATION NUMBER: US 09/710,150 PRIOR FILING DATE: 2001-07-18 PRIOR APPLICATION NUMBER: US 6/0/219,028 PRIOR FILING DATE: 2000-07-18 PRIOR APPLICATION NUMBER: US 10/251,507 PRIOR FILING DATE: 2002-09-20 PRIOR APPLICATION NUMBER: US 09/715,479 PRIOR FILING DATE: 2000-11-17 PRIOR APPLICATION NUMBER: US 6/0/218,053 PRIOR FILING DATE: 2000-07-13 PRIOR APPLICATION NUMBER: US 09/544,929 PRIOR FILING DATE: 2000-08-23 PRIOR APPLICATION NUMBER: US 6/0/212,439 PRIOR FILING DATE: 2000-06-16 PRIOR APPLICATION NUMBER: US 09/592,870 PRIOR FILING DATE: 2001-06-26 PRIOR APPLICATION NUMBER: US 6/0/214,174 PRIOR FILING DATE: 2000-06-26 PRIOR APPLICATION NUMBER: US 09/775,117 PRIOR FILING DATE: 2000-02-01 Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 156 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO: 131 LENGTH: 262 TYPE: PRT

RESULT 4 US-11-301-554-1812

; Sequence 1812, Application US/11301554
; Publication No. US20060088527A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Kalos, Michael D.
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Carter, Barrick
; APPLICANT: Sleath, Paul R.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.478621 CURRENT APPLICATION NUMBER: US/11/301,554 CURRENT FILING DATE: 2005-12-13 PRIOR APPLICATION NUMBER: US 10/283,017 PRIOR FILING DATE: 2002-10-28 PRIOR APPLICATION NUMBER: US 10/113,872 PRIOR FILING DATE: 2002-03-28 PRIOR APPLICATION NUMBER: US 10/017,754 PRIOR FILING DATE: 2001-10-29 PRIOR APPLICATION NUMBER: US 09/902,941 PRIOR FILING DATE: 2001-07-10 PRIOR APPLICATION NUMBER: US 09/849,626 PRIOR FILING DATE: 2001-05-03 PRIOR APPLICATION NUMBER: US 09/736,457 PRIOR FILING DATE: 2000-12-13 PRIOR APPLICATION NUMBER: US 09/702,705 PRIOR FILING DATE: 2000-10-30 PRIOR APPLICATION NUMBER: US 09/677,419 PRIOR FILING DATE: 2000-10-06 PRIOR APPLICATION NUMBER: US 09/671,325 PRIOR FILING DATE: 2000-09-26 PRIOR APPLICATION NUMBER: US 09/658,824 PRIOR FILING DATE: 2000-09-08 Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 2157 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO: 1812 LENGTH: 474 TYPE: PRT

RESULT 5 US-11-301-554-1812

; ORGANISM: Artificial sequence
; FEATURE: OTHER INFORMATION: Consensus amino acid sequence
; US-10-370-959-131

Query Match 8.3%; Score 64; DB 6; Length 262;
; Best Local Similarity 24.7%; Pred. No. 3.8; Mismatches 20; Indels 20; Gaps 2; Matches 20; Conservative 9; MisMatches 32; Indels 20; Gaps 2;

Qy 70 APGGIANP---EKKM-----NCGTOCPNSQSLSSGPTLKONGLWTB 109
Db 95 APAAFGNPQVLEKSLKGPHIEBYQLADAHGNCITLCNRACSDORGTRIKRSIEVAPSQ 154

RESULT 6 US-11-301-554-1812

; Sequence 1812, Application US/11301554
; Publication No. US20060088527A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Kalos, Michael D.
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Carter, Barrick
; APPLICANT: Sleath, Paul R.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.478621 CURRENT APPLICATION NUMBER: US/11/301,554 CURRENT FILING DATE: 2005-12-13 PRIOR APPLICATION NUMBER: US 10/283,017 PRIOR FILING DATE: 2002-10-28 PRIOR APPLICATION NUMBER: US 10/113,872 PRIOR FILING DATE: 2002-03-28 PRIOR APPLICATION NUMBER: US 10/017,754 PRIOR FILING DATE: 2001-10-29 PRIOR APPLICATION NUMBER: US 09/902,941 PRIOR FILING DATE: 2001-07-10 PRIOR APPLICATION NUMBER: US 09/849,626 PRIOR FILING DATE: 2001-05-03 PRIOR APPLICATION NUMBER: US 09/736,457 PRIOR FILING DATE: 2000-12-13 PRIOR APPLICATION NUMBER: US 09/702,705 PRIOR FILING DATE: 2000-10-30 PRIOR APPLICATION NUMBER: US 09/677,419 PRIOR FILING DATE: 2000-10-06 PRIOR APPLICATION NUMBER: US 09/671,325 PRIOR FILING DATE: 2000-09-26 PRIOR APPLICATION NUMBER: US 09/658,824 PRIOR FILING DATE: 2000-09-08 Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 2157 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO: 1812 LENGTH: 474 TYPE: PRT

RESULT 7 US-11-301-554-1812

; ORGANISM: Homo sapiens

RESULT 5
US-10-511-937-2464
; Sequence 2464, Application US/10511937
; Publication No. US2006008883641
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James B
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OR INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
FILE REFERENCE: 506612000104
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR FILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR FILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR FILING DATE: 2003-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: PatentIn version 3.2
SSQ ID NO 2464
LENGTH: 443
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2464

RESULT 6
US-10-505-928-784
; Sequence 784, Application US/10505928
; Publication No. US200600885241
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
FILE REFERENCE: 28967/3918
CURRENT APPLICATION NUMBER: US/10/505,928
CURRENT FILING DATE: 2004-08-27
PRIOR APPLICATION NUMBER: US 60/363,019
PRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 866
SOFTWARE: PatentIn 3.2
SEQ ID NO 784
LENGTH: 2671
TYPE: PRT
ORGANISM: Homo sapiens

RESULT 7
US-11-251-465-23
; Sequence 23, Application US/11251465
; Publication No. US20060094061A1
; GENERAL INFORMATION:
; APPLICANT: BRYB, Reginald
; APPLICANT: Vandeginste, Nick
; APPLICANT: Tomme, Peter
; APPLICANT: Klaassen, Hubertus
; TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The
TITLE OF INVENTION: Same, Useful In The Treatment Of Joint Degenerative And
TITLE OF INVENTION: Inflammatory Diseases
FILE REFERENCE: P30,172-A USA
CURRENT APPLICATION NUMBER: US/11/251,465
CURRENT FILING DATE: 2005-10-14
PRIOR APPLICATION NUMBER: 60/619,384
PRIOR FILING DATE: 2004-10-15
NUMBER OF SEQ ID NOS: 880
SOFTWARE: PatentIn version 3.3
SSQ ID NO 23
LENGTH: 404
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-251-465-23

RESULT 8
US-10-322-836-48
; Sequence 48, Application US/10322836
; Publication No. US2006009021A1
; GENERAL INFORMATION:
; APPLICANT: Turner, Alexander C., Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Neils, Michael
; APPLICANT: Friedrich, Glenn A.
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND PROTEINS
FILE REFERENCE: 8535-037-999
CURRENT APPLICATION NUMBER: US/10/322,836
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: US/09/579,114
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PatentSEQ For Windows Version 3.0
SEQ ID NO 48

RESULT 9
US-11-111-142-108
; Sequence 142, Application US/1111142
; Publication No. US2006009021A1
; GENERAL INFORMATION:
; APPLICANT: BRYB, Reginald
; APPLICANT: Vandeginste, Nick
; APPLICANT: Tomme, Peter
; APPLICANT: Klaassen, Hubertus
; TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The
TITLE OF INVENTION: Same, Useful In The Treatment Of Joint Degenerative And
TITLE OF INVENTION: Inflammatory Diseases
FILE REFERENCE: P30,172-A USA
CURRENT APPLICATION NUMBER: US/11/111,142
CURRENT FILING DATE: 2005-10-15
PRIOR APPLICATION NUMBER: 60/619,384
PRIOR FILING DATE: 2004-10-15
NUMBER OF SEQ ID NOS: 880
SOFTWARE: PatentIn version 3.3
SSQ ID NO 23
LENGTH: 404
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-111-142-108

RESULT 10
US-10-545-541-66
; Sequence 541, Application US/10545541
; Publication No. US2006009021A1
; GENERAL INFORMATION:
; APPLICANT: BRYB, Reginald
; APPLICANT: Vandeginste, Nick
; APPLICANT: Tomme, Peter
; APPLICANT: Klaassen, Hubertus
; TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The
TITLE OF INVENTION: Same, Useful In The Treatment Of Joint Degenerative And
TITLE OF INVENTION: Inflammatory Diseases
FILE REFERENCE: P30,172-A USA
CURRENT APPLICATION NUMBER: US/10/545,541
CURRENT FILING DATE: 2005-10-15
PRIOR APPLICATION NUMBER: 60/619,384
PRIOR FILING DATE: 2004-10-15
NUMBER OF SEQ ID NOS: 880
SOFTWARE: PatentIn version 3.3
SSQ ID NO 23
LENGTH: 404
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-545-541-66

RESULT 11
US-10-545-541-110
; Sequence 541, Application US/10545541
; Publication No. US2006009021A1
; GENERAL INFORMATION:
; APPLICANT: BRYB, Reginald
; APPLICANT: Vandeginste, Nick
; APPLICANT: Tomme, Peter
; APPLICANT: Klaassen, Hubertus
; TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The
TITLE OF INVENTION: Same, Useful In The Treatment Of Joint Degenerative And
TITLE OF INVENTION: Inflammatory Diseases
FILE REFERENCE: P30,172-A USA
CURRENT APPLICATION NUMBER: US/10/545,541
CURRENT FILING DATE: 2005-10-15
PRIOR APPLICATION NUMBER: 60/619,384
PRIOR FILING DATE: 2004-10-15
NUMBER OF SEQ ID NOS: 880
SOFTWARE: PatentIn version 3.3
SSQ ID NO 23
LENGTH: 404
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-545-541-110

RESULT 12
US-10-545-541-76
; Sequence 541, Application US/10545541
; Publication No. US2006009021A1
; GENERAL INFORMATION:
; APPLICANT: BRYB, Reginald
; APPLICANT: Vandeginste, Nick
; APPLICANT: Tomme, Peter
; APPLICANT: Klaassen, Hubertus
; TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The
TITLE OF INVENTION: Same, Useful In The Treatment Of Joint Degenerative And
TITLE OF INVENTION: Inflammatory Diseases
FILE REFERENCE: P30,172-A USA
CURRENT APPLICATION NUMBER: US/10/545,541
CURRENT FILING DATE: 2005-10-15
PRIOR APPLICATION NUMBER: 60/619,384
PRIOR FILING DATE: 2004-10-15
NUMBER OF SEQ ID NOS: 880
SOFTWARE: PatentIn version 3.3
SSQ ID NO 23
LENGTH: 404
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-545-541-76

RESULT 13
US-10-545-541-202
; Sequence 541, Application US/10545541
; Publication No. US2006009021A1
; GENERAL INFORMATION:
; APPLICANT: BRYB, Reginald
; APPLICANT: Vandeginste, Nick
; APPLICANT: Tomme, Peter
; APPLICANT: Klaassen, Hubertus
; TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The
TITLE OF INVENTION: Same, Useful In The Treatment Of Joint Degenerative And
TITLE OF INVENTION: Inflammatory Diseases
FILE REFERENCE: P30,172-A USA
CURRENT APPLICATION NUMBER: US/10/545,541
CURRENT FILING DATE: 2005-10-15
PRIOR APPLICATION NUMBER: 60/619,384
PRIOR FILING DATE: 2004-10-15
NUMBER OF SEQ ID NOS: 880
SOFTWARE: PatentIn version 3.3
SSQ ID NO 23
LENGTH: 404
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-545-541-202


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; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-0-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 458
; LENGTH: 734
; TYPE: PRT
; ORGANISM: Homo sapien
; US-10-196749-458

RESULT 12
Query Match          7.8%; Score 59.5; DB 6; Length 734;
Best Local Similarity 30.4%; Pred. No. 48; Mismatches 27; Indels 13; Gaps 5;
Matches 24; Conservative 15; Mismatches 27; Indels 13; Gaps 5;
Qy      33 SDALPSAATDS--GPEAG--GHAGVIEDGPSNGVLRPAAPGGIANPEKKGKNCGTQC 87
Db      126 SDRSLLEASSQSGFGLGPHGRNLHSG--LEDGDYDGM--CAEQDADPWFQVDAG--- 179
Qy      88 PNSOSSLSSCPLTOKONGLW 106
Db      180 -HPTTRPFGVITQGRNSVW 196

RESULT 13
US-10-538-066-363
Sequence 363, Application US/10538066
Publication No. US20060094649A1
; GENERAL INFORMATION:
; APPLICANT: Biimmune Inc.
; TITLE OF INVENTION: HLA-A1, -A2, -A3, -A24, -B7, and -B44 Tumor Associated Antigen
; FILE REFERENCE: 2060_015PC06
; CURRENT APPLICATION NUMBER: US/10/538,066
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US 60/432,017
; PRIOR FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 757
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 363
; LENGTH: 702
; TYPE: PPT
; ORGANISM: Homo sapiens
; US-10-538-066-363

RESULT 14
US-11-169-140-14
Sequence 14, Application US/11169140
; Publication No. US20060099150A1
; GENERAL INFORMATION:
; APPLICANT: ARIZEKE PHARMACEUTICALS, INC.
; TITLE OF INVENTION: METHODS FOR THE TRANSPORT OF BIOLOGICALLY ACTIVE AGENTS ACROSS CELL BARRIERS
; FILE REFERENCE: 11474-037-959
; CURRENT APPLICATION NUMBER: US/11/169,140
; CURRENT FILING DATE: 2005-06-27
; PRIOR APPLICATION NUMBER: US 60/267,601
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/248,819
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/248,478
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: US 60/237,929
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 09/949,039
; PRIOR FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: 09/969,748
; PRIOR FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.0
; US-10-196749-458

Qy      83 C--GTQCPNSQSLSSGPILTOKONGLWTEAKRDA--KRMSSAREVATSV-----TP 128
Db      449 WLIDGNICDQHTOBULFISHNTERKNSGlyCQANNNSASGHSTTVKTTTSABLKPSSIIN 508
Qy      129 NIRDMDRSKRVTRNC 143
Db      509 NSKVEDKDVAFTC 523

RESULT 15
US-10-505-928-831
Sequence 831, Application US/10505928
; Publication No. US2006008532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 2867/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 831
; LENGTH: 2026
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-505-928-831

RESULT 16
US-10-505-928-831
Sequence 831, Application US/10505928
; Publication No. US2006008532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 2867/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 831
; LENGTH: 2026
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-505-928-831

RESULT 17
US-11-169-140-14
Sequence 14, Application US/11169140
; Publication No. US20060099150A1
; GENERAL INFORMATION:
; APPLICANT: HOUSTON, Lou, L.
; APPLICANT: SHERIDAN, Philip, J.
; APPLICANT: HAWLEY, Stephen
; APPLICANT: GLANN, Jacqueline, M.
; APPLICANT: CHAPIN, Steven
; TITLE OF INVENTION: BARRIERS
; FILE REFERENCE: 11474-037-959
; CURRENT APPLICATION NUMBER: US/11/169,140
; CURRENT FILING DATE: 2005-06-27
; PRIOR APPLICATION NUMBER: US 60/267,601
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/248,819
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/248,478
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: US 60/237,929
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 09/949,039
; PRIOR FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: 09/969,748
; PRIOR FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.0
; US-10-196749-458

Qy      6 SRADAEPPYYESWTRETE--STWLTYDSDALP-----SAATDSG 45
Db      330 NNSNPVERBDAVALTCEPIQNTYIWWNNQSLPVSPRIQLQSNDRNLTLSVTRDVG 389
Qy      46 PEAGGLHAGVTL-----GPSENGVLREA---APG-----GIANPEKKG 82
Db      390 PYEGQJONBLSVDHSDPVLNVLYGP--DDPTISPYTYRPGVNLISCHAASNPQAOS 448

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; SEQ ID NO 14
; LENGTH: 663
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-11-169-40-14

Query Match 7.6%; Score 58.5; DB 7; Length 663;
Best Local Similarity 24.0%; Pred. No. 54; Matches 18; Conservative 11; Mismatches 31; Indels 15; Gaps 1;
Matches 18; Conservative 11; Mismatches 31; Indels 15; Gaps 1;

QY      38 SAAATDGPPEAGCILHAGVLEDDGSPSSNGVLRPAAPGGTANPEKKNCGTQCPNSQSLSGP 97
Db      211 NWATSDQOKPKRAKRGV-----PGELATPDKENDAKSSDSVGEBELP 255
QY      98 L'RKONGIWTTRAKER 112
Db      256 SSSLKSGKVKVDAEK 270

RESULT 15
US-10-505-928-569
; Sequence 569, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 2896739178
; CURRENT APPLICATION NUMBER: US/10/505, 928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/3363, 019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 569
; LENGTH: 4590
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-505-928-569

Query Match 7.6%; Score 58.5; DB 6; Length 4590;
Best Local Similarity 21.6%; Pred. No. 7.4e+02;
Matches 27; Conservative 23; Mismatches 56; Indels 19; Gaps 5;
Matches 27; Conservative 23; Mismatches 56; Indels 19; Gaps 5;

QY      22 ETEST---WLTV--TDSDALPAA-----ATSGPPEAGG-LHAGVLEDDGSSNG 64
Db      1098 DRETSIHWLTLFATDQCVWPLSSPFIEVIEDVNNDAPQSEPVVPEIENNSPKDV 1157
QY      65 VVRAAAGGIAPEKKNGTCOPNSQSLSSPLTQKONGLWTEAKRDAKMSAREVAI 124
Db      1158 VVQIEAFDPDSSNDKLMVKITISGNPOQFFS-IHPKTGLITTSRKLDRQQDEHLEV 1215
QY      125 SYTEN 129
Db      1216 TTYDN 1220

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Search completed: May 20, 2006, 21:23:46
Job time : 5 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: May 20, 2006, 21:06:32 ; Search time 38 Seconds
(Without alignments)

367.143 Million cell updates/sec

Title: US_10-705-716a-2

Perfect score: 767

Sequence: 1 MGCGGSRRADATEPRVYYSWT.....VTEENIRQMDRSKRVTKCIN 145

Scoring table: BLOSUM62

Gapop 10.0 , Gapext: 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80;*

1: pir1;*
2: pir2;*
3: pir3;*
4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Length DB ID

Description

Result No.	Score	Query	Length	DB	ID
1	92.5	12.1	571	2	T43456
2	92.5	12.1	778	2	A35970
3	88	11.5	365	1	GNVSSC
4	83	10.8	1433	2	S554587
5	81	10.6	269	2	T37073
6	81	10.6	967	2	S66852
7	79.5	10.4	2559	2	T09144
8	78.5	10.2	1199	2	A40670
9	78	10.2	885	2	T09225
10	78	10.2	3488	2	T34418
11	76.5	10.0	600	2	C66899
12	76	9.9	645	2	S19156
13	76	9.9	839	2	E84824
14	75.5	9.8	499	2	S22571
15	75.5	9.8	1063	2	T03743
16	75.5	9.8	1122	2	T47424
17	75	9.8	368	1	TVM3H
18	75	9.8	521	2	I15193
19	74.5	9.7	601	2	AH0784
20	74.5	9.7	4957	2	T0355
21	74.5	9.7	5262	2	T0354
22	74	9.6	260	2	B38594
23	74	9.6	742	2	T38001
24	74	9.6	832	2	T31878
25	74	9.6	2	T0262	
26	73.5	9.6	876	1	A57988
27	73.5	9.6	960	2	T37916
28	73.5	9.6	1575	2	S68418
29	73	9.5	1575	2	H98327

ALIGNMENTS

RESULT 1

T43456 hypothetical protein DKPZp34L061.1 - human

C;Species: Homo sapiens (man)
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43456
R;Fousta, A.; Klein, M.; Mewes, H.-W.; Gasenhuber, J.; Wiemann, S.
Submitted to the Protein Sequence Database, December 1999

A;Reference number: 222516
A;Accession: T43456
A;Status: preliminary

A;Molecule type: mRNA
A;Residues: 1-571 <AAA>

A;Cross-references: UNIPROT:O75175; UNIPARC:UPI000006PFE9; EMBL:AL133647
A;Experimental source: adult testis; Clone DKPZp34L061

C;Genetics: C;Note: DKPZp434L061.1
C;Superfamily: hydroxyproline-rich glycoprotein

Query Match Best Local Similarity 12.1%; Score 92.5; DB 2; Length 571;
Matches 30; Conservative 31.9%; Pred. No. 0; 92; Mismatches 32; Indels 25; Gaps 3;

QY 31 TDSDALPRAATDGSPEAGGLH-----AGVIEDGSSNGVLRPAAD-- 71
Db 111 TDSEVSOSPAKNGSKPVNSQHQFQSPAVPTFSGPPPPASAISITPENNPGTPAPAPS 170
QY 72 --GGIANPERKKOMCGTCCPNPSLS---SGPLT 99
Db 171 ALGPKASPAHSNNSGTPAPYQAQAVAPPAPSGPST 204

RESULT 2

glutamyl-tRNA amid
hypothetical prote
enamelin matrix pr
cytochrome-related
transcription fact
preplin [imported
probable soluble-bi
ilinase (EC 3.2.
cell division prot
intrinsic factor-B
microtubule-associ
hypothetical prote
DNA-directed DNA p
DNA Polymerase del
3-dehydroquonate s
8-amino-7-oxononan

A35970 erythrocyte-binding protein - Plasmodium knowlesi
C;Species: Plasmodium knowlesi
C;Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 09-Jul-2004
C;Accession: A35970
R;Adams, J.R.; Hudson, D.B.; Torii, M.; Ward, G.B.; Wellens, T.E.; Aikawa, M.; Miller,
Cell 63, 141-153, 1990
A;Title: The duffy receptor family of plasmodium knowlesi is located within the micron
A;Reference number: A35970; MUID:91004213; PMID:2170017
A;Accession: A35970
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-778 <AAA>
A;Cross-references: UNIPR0N:P22545; UNIPARC:UPI000016BPA8; GB:M68518; GB:M37513; NID:91
C;Keywords: transmembrane protein

Query Match Best Local Similarity 12.1%; Score 92.5; DB 2; Length 778;
Matches 29; Conservative 12; Mismatches 44; Indels 3; Gaps 3;

RESULT 3

GNVSSC

Genome polyprotein - sugarcane mosaic virus (strain SC) (fragment)

N;Contains: carboxyl end of nuclear inclusion protein b; coat protein

C;Species: *Saccharomyces cerevisiae*

C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004

C;Accession: PH0207

R;Frenkel, M.J.; Jikka, J.M.; McKern, N.M.; Strike, P.M.; Clark Jr., J.M.; Shukla, D.D.; J. Gen. Virol. 72, 237-242, 1991

A;Title: Unexpected sequence diversity in the amino-terminal ends of the coat proteins of *Saccharomyces cerevisiae*

A;Reference number: PH0207; MUID:91132116; PMID:1993866

A;Accession: PH0207

A;Molecule type: genomic RNA

A;Residues: 1-365 <PRE>

A;Cross-references: UNIPROT:P25242; UNIPARC:UP1000131E72; GB:D00948; NID:922123; PIDN: C;Superfamily: tobacco etch virus genome polyprotein

C;Keywords: coat protein; inclusion protein

F;52-Product: nuclear inclusion protein b (fragment) #status predicted <COA>

F;53-365/Product: coat protein #status predicted <COA>

Query Match 11-5*: Score 88; DB 1; Length 365;

Best Local Similarity 21.6%; Pred. No. 14; Matches 30; Conservative 24; Mismatches 79; Indels 6; Gaps 4;

QY 5 GSRADDAIEPRVYESWWRTEESTWLTYTDSALPSAAATDGPBAGGLHAGVL--EDGSS 62

Db 21 GITKEESE-EKFQKPAFDKGDPGYLDVND-EVHQAGTVDAGQGGGENAGTOPPAGAA 78

QY 63 NGVLRLPAPGGTANPEKKNNCGTQCPNSOSLSSGGL-TOKONGLWTEAKRDKRMAREV 122

Db 79 QGGAQPATGAAQPPHQ-GSQLPOGATGGGAQTGAGGTGSVTOGQDKDVAGTT 136

QY 123 AISVTUNIQRDRSKRTV 141

Db 137 GKITVPUKLUKAMSKKMRUPK 155

RESULT 4

S54587

CAT8 protein - Yeast (*Saccharomyces cerevisiae*)

N;Alternate name: MsP8 protein; protein YMR280c

C;Species: *Saccharomyces cerevisiae*

C;Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 05-Oct-2004

C;Accession: S54587; S48234; S61595; S49498

R;Pearson, D.; Bowman, S.

submitted to the EMBL Data Library, May 1995

A;Reference number: S54582

A;Accession: S54587

A;Molecule type: DNA

A;Residues: 1-1433 <PEA>

A;Cross-references: UNIPROT:P9113; UNIPARC:UP100012704; EMBL:249704; NID:982540; PIDN: R;Grebitza, D.

submitted to the EMBL Data Library, March 1994

A;Reference number: S48234

A;Accession: S48234

A;Molecule type: DNA

A;Residues: 1-746, 'L', 748-1433 <GRZ>

A;Cross-references: UNIPARC:UP1000168B45; EMBL:X78344; NID:9559523; PIDN:CAA55139.1; PI submitted to the EMBL Data Library, December 1995

A;Reference number: S61594

A;Accession: S61595

submitted to the Protein Sequence Database, July 1996

A;Reference number: S66854

A;Accession: SG6854

A;Molecule type: DNA

A;Residues: 1-167 <ORI>

A;Experimental source: brain S288C

R;Gamo, F.J.; Lafuente, M.J.; Casamayor, A.; Aldea, M.; Casas, C.; Ario, J.; Herrero, E.

submitted to the EMBL Data Library, July 1995

A;Description: Analysis of the DNA sequence of a 15500 bp fragment of the left arm of ch

pen reading frames.

A;Reference number: S67324

A;Accession: S67325

A;Molecule type: DNA

A;Residues: 1-164, 'STTSITGGSSATESGGSVSGSTSATSGSSAGSS', 166-186, 'V', 188-967 <GAM>

A;Cross-references: UNIPARC:UPI00006C5C2; EMBL:Z74897; NID:91420063; PID:e251930; PID:q

R;Gamo, F.J.; Lafuente, M.J.; Casamayor, A.; Aldea, M.; Casas, C.; Ario, J.; Herrero, E.

Yeast 12, 709-714, 1996

A;Title: Analysis of the DNA sequence of a 15,500 bp fragment near the left telomere of

and two new open reading frames.

A;Reference number: S70379; MUID:96405919; PMID:881004

A;Accession: S70380

A;Status: nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 55-164, 'STTSITGGSSATESGGSVSGSTSATSGSSAGSS', 166-186, 'V', 188-286, 'G', 287-745, 'T', 746-781

A;Cross-references: UNIPARC:UPI000017CCC3; UNIPARC:UPI000017CCC4; UNIPARC:UPI000017CCC5;

C;Genetics: A;Cross-references: SGD:S0005515

A;Map position: 15L

A;Note: YOL153C

Query Match 10.6%; Score 81; DB 2; Length 967;

Best Local Similarity 24.8%; Pred. No. 20; Mismatches 29; Conservative 23; Gaps 2; Indels 10; Gaps 2;

Matches 55; Query Match 17 ESMWETESTWLTIVDSDAISMAATDSRERGG---IHNQVLEDPSGSQVLRPAAGC 72

Db 182 ESGSSASGSSATESGSSVSVSSSATESGSSVSVSSSATESGSSASSVSPSSGVSITESGS 241

QY 73 GIANIEKRMNGTQCPNSQSISSGSPILTKQONGLWTTEAKRDIAKRMSSAREVAINSYEN 129

Db 242 SSASISSITQSGTAGCASSSSTSGVQSGSSVSVSSSAS---SAPGISSIPQS 292

RESULT 7

T09144 probable guanine nucleotide exchange factor RhoGFP2 - fruit fly (*Drosophila melanogaster*)

C;Species: *Drosophila melanogaster*

C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C;Accession: T09144; T09223

R;Haecker, U.; Perrimon, N. Library, submitted to the EMBL Data Library, October 1997

A;Reference number: Z16586

A;Accession: T09144

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-2259 <HAE>

A;Cross-references: UNIPROT:O44113; UNIPARC:UPI00007F684; EMBL:AF031930; NID:92687355;

R;Bartlett, K.; Lepin, M.; Settleman, J.

CeII, 91, 905-915, 1997

A;Title: The Rho GTPase and a putative RhoGFP mediate a signaling pathway for the cell s

A;Reference number: Z16618; MUID:98088790; PMID:9428514

A;Accession: T09223

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-676, 'L', 678-837, 'L', 839-889, 'S', 891-1233, 'D', 1245-1358, 'E', 1360-1368, 'R', 1

A;Cross-references: UNIPARC:UPI000007D45E; EMBL:AF032870; NID:92760367; PID:NAC38820.1;

C;Genetics: A;Cross-references: FlyBase:FBgn0023172

A;Map position: 2; 53F1-2

C;Function:

A;Description: mediates actin rearrangements required for cell shape changes during ga

C;Superfamily: rat Munc-13-3 protein; protein kinase C zinc-binding repeat homology

C;Domain: embry; signal transduction; signal transduction

R;1151-1200/Domain: protein kinase C zinc-binding repeat homology <K2N>

Query Match 10.4%; Score 79.5; DB 2; Length 2559;

Best Local Similarity 28.3%; Pred. No. 83; Mismatches 30; Conservative 11; Gaps 9; Indels 9; Gaps 3; Matches 56; Query Match 5 GSRADAIERPIVYESWTERSTWLTIVDSDAISMAATDSRERGG---IHNQVLEDPSGSQVLRPAAGC 64

Db 799 GSSPDNMHRPHDRITKTTSQSW-EIVERKDGESSPPGTTPPPVYLSHMTVLEDPNENN 857

QY 65 VLRLPAAPI-GIANIEKRMNGTQCPNSQSISSGSPILTKQONGLWTTEAKRDIAKRMSSAREVAINSYEN 102

Db 858 GAAAAGPGPVIESHOFPTMAGASSPIPISPLSHNMHAQNDTQE 903

RESULT 8

A;Accession: A40670

A;Status: preliminary; nuclear envelope protein POM 121 - rat

C;Species: *Rattus norvegicus* (Norway rat)

C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004

R;Hallberg, B.; Wozniak, R.W.; Blobel, G.

J. Cell Biol. 122, 513-521, 1993

A;Title: An integral membrane protein of the pore membrane domain of the nuclear envelop

A;Reference number: A40670; MUID:93320754; PMID:8335683

A;Accession: A40670

A;Status: preliminary; mRNA

A;Residues: 1-1199 <HAI>

A;Cross-references: UNIPROT:P52291; UNIPARC:UPI000012FC0B; GB:Z21513; NID:9396746; PID:F

F;803-807, 845-849, 956-960, 1010-1014, 1047-1051, 1076-1080/Region: pentapeptide motif (X-)

Query Match 10.2%; Score 78.5; DB 2; Length 1199;

Best Local Similarity 25.2%; Pred. No. 43; Mismatches 39; Conservative 19; Gaps 56; Indels 41; Gaps 6; Matches 39; Query Match 20 TREPSTWLTIVDSDAISMAATDSRERGG---AATDGPSPAGGLHAQVLEDPSSNGVLRPAAGCA- 75

Db 363 SRTSNSVSLTSTCGGSSRNNAITSSYNSSTRGVSQWIKRSRGPSSPPSSPSSRSPR 422

QY 76 -NPRAKRMNGTQCPNSQSISSGSPILTKQONGLWTTEAKRDIAKRMSSAREVAINSYEN 111

Db 423 BRPAKTR--BRBRHQSSSAPIVTDKPSGKVTDATGKQSLWTSPPGSSQRK 480

QY 112 RDAKRMSA-----EVAVTNIROHDR 135

Db 481 RKLQLPSPRRGDQLTLPPPELGYSITADELDWME 515

RESULT 9

T09225

A;kinase anchor protein AKAP-KL isoform 1 - mouse

C;Species: Mus musculus (house mouse)

C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C;Accession: T09225; T09226; T09227

R;Bong, F.; Feldmesser, M.; Casdevall, A.; Rubin, C.S.

J. Biol. Chem. 273, 6533-6541, 1998

A;Title: Molecular characterization of a cDNA that encodes six isoforms of a novel mur

A;Reference number: 216620; MUID:98165844; PMID:9497389

A;Accession: T09225

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-885 <DO2>

A;Cross-references: UNIPROT:O54931; UNIPARC:UPI000028356; EMBL:AF033274; NID:92852696;

C;Genetics: A;Note: binds the regulatory subunits (RI) of protein kinase AII isoforms

A;Accession: T09226

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-848, 862-885 <DO2>

A;Cross-references: UNIPARC:UPI00002A38B; EMBL:AF033275; NID:9282698; PID:92852699
 A;Note: binds the regulatory subunits (RII) of protein kinase RII isoforms
 A;Accession: T09227
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: mRNA
 A;Residues: 1-789; PGEMTG_<D03>
 A;Cross-references: UNIPARC:UPI000027DD; EMBL:AF033276; NID:92852700; PID:92852701
 A;Note: binds the regulatory subunits (RII) of protein kinase RII isoforms
 C;Genetics:
 A;Gene: AKAP-KL
 C;Keywords: alternative splicing; kidney; lung; signal transduction
 Query Match 10.2%; Score 78; DB 2; Length 885;
 Best Local Similarity 29.6%; Pred. No. 33; Mismatches 33; Indels 32; Gaps 7;
 Matches 34; Conservative 16; Mismatches 33; Indels 32; Gaps 7;
 Qy 49 GGLHAGVLEDGPGSSNGVLRPAAPGGI-----ANPEKKKNCCTQCQCPNSQSLSGP--L 98
 Db 381 GS1HS---DKPPT---ILRPLATVGTLEDGGTQAKEQKAPPVSE--SQCAGPANAA 431
 Qy 99 TKOKNGLWTEAKR-----DAKRMSAREVAISVTEN---IRQMDRSKRV 140
 Db 432 TQGKEGPISSEPSKRKGPLSKLWAERGEFTSARRAVITVVKDQEDHGILDQFSRSVIVS 486
 RESULT 10
 hypothetical protein F12F3_3 - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 C;Accession: T34418
 R;Fulton, B.; Wohldmann, P.
 Submitted to the EMBL Data Library, July 1998
 Description: The sequence of C. elegans cosmid F12F3.
 A;Reference number: Z21521
 A;Accession: T34418
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Experimental source: strain Bristol N2; clone F12F3
 A;Cross-references: UNIPARC:UPI000017B8E6; EMBL:U80022; PIDN: AAC25885.1; GSPDB:GN00023;
 C;Genetics:
 A;Gene: CESP_F12F3_3
 A;Map position: 5
 A;Introns: 281/3; 332/1; 562/3; 600/3; 1866/3; 1944/3; 3393/1
 Query Match 10.2%; Score 78; DB 2; Length 600;
 Best Local Similarity 23.1%; Pred. No. 29; Mismatches 56; Indels 51; Gaps 7;
 Matches 39; Conservative 23; Mismatches 56; Indels 51; Gaps 7;
 Qy 9 DATEPRYEVSWTRB-----TESTWLYTDPSALPSAATDSGPRAEGGLHAGVLEOPS 61
 Db 342 DAISAAEESTYQKDMVNGDAYSRSRWTVY---AIGSVAVATVGTKG---AGAINKDA 393
 Qy 62 SNGVLRPAPGGTA-----NEBEKKKNCGTQCP---NSQSLSSGPIT----- 99
 Db 394 AGKVINKKSQAGKKIKWKIPDLPYKPKYKLADNPVNVDSDQNLNEELTNACKP 453
 Qy 10 -----OKONGLWTEAKRDAKRMSAREVAISVTENIRQMDRSKRV 119
 Db 454 DGTTRKPPFGQKUSPPWLNEKYD-----AYEIEGKVICKGKVKDVSRRV 497
 RESULT 12
 S19156
 Serotonin receptor 2B - fruit fly (*Drosophila melanogaster*)
 N;Alternate names: 5-hydroxytryptamine receptor 2B (5-HTR2B)
 C;Species: *Drosophila melanogaster*
 C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
 C;Accession: S19156; S18154
 R;Saoudou, F.; Boschert, U.; Amaliaky, N.; Plassat, J.L.; Hen, R.
 EBO J. 11, 7-17, 1992
 A;Title: A family of *Drosophila* serotonin receptors with distinct intracellular signal
 A;Reference number: S19155; MUID:92155185; PMID:1310937
 A;Accession: S19156
 A;Molecule type: mRNA
 A;Residues: 1-645 <SAI>
 A;Cross-references: UNIPROT:P28286; UNIPARC:UPI000124F41; EMBL:Z11490; NID:97506; PID:
 C;Genetics:
 A;Gene: FlyBase:5-HTB
 A;Cross-references: FlyBase:FBgn004572
 C;Superfamily: G protein-coupled receptor type I
 C;Keywords: octopamine receptor; glycoprotein; transmembrane protein
 F124-145/Domain: transmembrane #status predicted <TM1>
 F1156-177/Domain: transmembrane #status predicted <TM2>
 F1193-214/Domain: transmembrane #status predicted <TM3>
 F123-256/Domain: transmembrane #status predicted <TM4>
 F1284-305/Domain: transmembrane #status predicted <TM5>
 F1564-587/Domain: transmembrane #status predicted <TM6>
 F1597-619/Domain: transmembrane #status predicted <TM7>
 C;Species: *Bacillus subtilis*
 C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 05-Oct-2004
 C;Accession: C69899
 R;Kunst, R.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berger, C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho A.; Bhilich, S.D.; Dunnison, P.T.; Entian, K.D.; Brington, J.; Fabret, C.; Ferrari, E.; Nature 390, 249-256, 1997
 Query Match 9.9%; Score 76; DB 2; Length 645;
 Best Local Similarity 31.0%; Pred. No. 35; Mismatches 31; Indels 26; Gaps 4;
 Matches 31; Conservative 12; Mismatches 31; Indels 26; Gaps 4;
 Qy 29 TYRSDAPSAATDSGPRAEGGLHAGVLEDGSSNGVLRPAAPGG----IANPEKKKNC 84
 Db 2867 TTEAEEV-KTKKKVVK 2881
 RESULT 11
 C9899
 conserved hypothetical protein yob1 - *Bacillus subtilis*
 C;Species: *Bacillus subtilis*

Db 489 TTPSEKALSGAGTVAGAVAGVAGSGSGSGSGSGGGAGTAGKNGAVGIGCLASIANPHQKL--- 545

Qy 85 TQCPNSQSLSSGPLTOKQNLWTTAKRDARKMSAREVAI 124

Db 546 - -----AKRQL--LEAKRE--RKAQTIAI 566

RESULT 13

E84824 hypothetical protein At2g40040 [imported] - Arabidopsis thaliana

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C;Accession: E84824

R;Lin, X.; Kaul, S.; Rounseley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Talon, I.; euse, D.; Niemant, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: E84824

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-839 <STO>

C;Cross-references: UNIPROT:004207; UNIPARC:UPI0000AB62E; GB:AE02093; NID:92088657; PI

A;Gene: At2g40040

A;Map position: 2

Query Match 9.9%; Score 76; DB 2; Length 839;

Matches 40; Conservative 14; Mismatches 62; Indels 52; Gaps 6;

Qy 5 GSRADATEPRYYESWTR-----ETESTWLTYTDALPSAA----- 41

Db 338 GSGACVLGP----WNKKSESETESGATGQSSDKTKSGAAMANSWDKKNIETDSEPAAWG 392

Oy 42 -----TDSGPRAAGGL---HAGVLEDGPSPSNQY-----LRPAPGCTANPEKEM 81

Db 393 S QGKKNSETESGPRAWGAWDKKKSBTEPGPAGWGNGDKKNSTELGPAAAGNNDDKKSDT 452

Qy 82 NCCTQCPNSQSLSSGPLTOKQNLWTTAKRDARKMSAREVAI 129

Db 453 KSGPAAWSSTDAAWGSSDKNN----SETESDAAAWGSRNKTKSEIES 496

RESULT 14

S22571 integrase-like protein FE65 - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 31-Dec-1993 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004

C;Accession: S22571; S22572

R;Duilio, A.; Zambrano, N.; Mogavero, A.R.; Ammendola, R.; Cimino, F.; Russo, T.

Nucleic Acids Res 19, 5269-5274, 1991

A;Title: A rat brain mRNA encoding a transcriptional activator homologous to the DNA binding protein

A;Reference number: S22571; MUID:92020215; PMID:1923810

A;Accession: S22571

A;Molecule type: mRNA

A;Residues: 1-499 <DUTI>

A;Cross-references: UNIPROT:Q99MK3; UNIPARC:UPI000170BC8; EMBL:X60469; NID:957559; PID:

A;Accession: S22572

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 31-318 <DUTI>

A;Cross-references: UNIPARC:UPI000170BC9; EMBL:X60468; NID:957561; PID:CAA42998.1; PID

A;Note: this sequence was submitted to the EMBL Data Library, July 1991

C;Genetics: C;Introns: 88/3; 107/3; 135/3; 157/3; 207/3; 250/2; 252/2; 290/3

C;Keywords: transcription regulation

F;42-78/Domain: WW repeat homology <WW1>

Query Match 9.8%; Score 75.5; DB 2; Length 499;

Best Local Similarity 25.6%; Pred. No. 29;

Matches 34; Conservative 17; Mismatches 59; Indels 23; Gaps 5;

Qy 13 PRYTESWTRTESTIWLTVDSDALPSAAITDSOPRAGGLHAGVLEDGPSNGVLRPAAG 72

Db 77 PSQGNSPRSPEQTLWTGP-----AHQGPFERGERP---WKDEBEBAMEL--- 118

Qy 73 GIANPEKQKNCGTOCPNSQSLSSGPLTOKQNLWTTAKRDARKMSAREVAI-SVTENR 131

Db 119 GLKDPEB---GLPFSQSLSPEPVFQEENLPQRMANPGIKCPAVTSIGNWEMTERBL 174

Qy 132 QMRSKRVTKNCI 144

Db 175 APGRSSVAVNCl 187

RESULT 15

T03743 bifocal protein - fruit fly (Drosophila melanogaster)

C;Species: Drosophila melanogaster

C;Accession: T03743 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004

C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004

R;Bahri, S.M.; Yang, X.Y.; Chia, W.

Mol. Cell. Biol. 17, 5521-5529, 1997

A;Title: The Drosophila bifocal gene encodes a novel protein which colocalizes with act

A;Reference number: Z15048; MUID:97415628; PMID:9271427

A;Accession: T03743

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-1063 <BAH>

A;Cross-references: UNIPROT:016125; UNIPARC:UPI00017B7D; EMBL:AF011791; NID:92398667;

C;Genetics:

A;Cross-references: FlyBase:FBgn0014133

A;Note: bifocal

Query Match 9.8%; Score 75.5; DB 2; Length 1063;

Matches 39; Conservative 23; Mismatches 59; Indels 67; Gaps 6;

Qy 5 GSRADATEPRYYESWTR-----ETESTWLTYTDALPSAA----- 42

Db 83 GATADPFTPATISCSORRNMGSEEKEKSISINTNSDTSGHHHSVAVSLSPDAAATT 142

Oy 43 -----DGSPEAEGHLAGVLEDGSNSNGVLRPAAG 72

Db 143 NWVVTPIPKQRSLLNTRSQEREWVRLTILSESERDLSERLSERBQPGTVNSRSGENETG 202

Qy 73 GIANPEKQKNCGTOCPNSQSLSSGPLTOKQNLWTTAKRDARKMSAREVAI 132

Db 203 TIGSPSSAN---QNPNEHLK---TRCKPGOSVABGKPSAK-----TIVUNSK 247

Qy 133 MDRSKRT 140

Db 248 CSKTKSIS 255

Search completed: May 20, 2006, 21:07:20
Job time : 40 Secs